OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: June 2, 2005, 11:24:52 ; Search time 25 Seconds
(without alignments)
1672.139 Million cell updates/sec

Title: US-10-734-731-4
Perfect Score: 2970
Sequence: 1 MEFRQEEFRKLAGRALGKLH.........YGATHSTFQPPRPPPVPVRDY 560

Scoring table: BLOSUM62
Scoring: Gapop 10.0 , Gapext 0.5
Searched: 513545 seqs, 74649064 residues

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcodata/1/iaa/backfiles1.pep:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters: 513545

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2970	100.0	560	1	US-08-647-484-2	Sequence 2, Appli...
2	2970	100.0	560	1	US-08-647-481-2	Sequence 2, Appli
3	2970	100.0	560	1	US-08-430-033A-2	Sequence 2, Appli
4	2970	100.0	560	5	PCT-US96-05792-2	Sequence 2, Appli
5	2962	99.7	567	5	PCT-US96-05792-2	Sequence 11354, A
6	2925	98.5	560	2	US-09-949-016-11354	Sequence 11354, A
7	2925	98.5	560	3	US-08-805-118-4	Sequence 4, Appli
8	2925	98.5	560	3	US-09-391-958-4	Sequence 4, Appli
9	2313.5	77.9	578	4	US-09-915-181A-5	Sequence 5, Appli
10	2313.5	77.9	582	4	US-09-740-041-4	Sequence 4, Appli
11	2185	73.6	589	4	US-09-915-181A-4	Sequence 4, Appli
12	2174.5	73.2	850	4	US-09-740-041-2	Sequence 2, Appli
13	1297	43.7	576	3	US-08-864-785-1	Sequence 3, Appli
14	1294	43.6	563	4	US-09-915-181A-6	Sequence 6, Appli
15	940	31.6	495	4	US-09-359-167-2	Sequence 2, Appli
16	940	31.6	495	4	US-09-915-181A-7	Sequence 7, Appli
17	940	31.6	536	4	US-09-359-167-8	Sequence 8, Appli
18	931	31.6	585	4	US-09-949-016-7705	Sequence 7705, Ap
19	931	31.3	495	4	US-09-359-167-4	Sequence 4, Appli
20	746	25.1	552	4	US-09-270-767-45540	Sequence 45540, A
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22	636.5	21.4	495	4	US-09-949-016-6616	Sequence 6616, Ap
23	636.5	21.4	495	4	US-09-359-167-12	Sequence 12, Appl
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25	626.5	21.1	467	4	US-09-391-958-3	Sequence 3, Appli
26	620	20.9	480	2	US-08-724-394A-9	Sequence 9, Appl
27	615	20.7	465	4	US-09-915-181A-8	Sequence 8, Appli
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41	322.5	10.9	234	4	US-09-489-039A-45527	Sequence 45527, A
42	322.5	10.9	434	4	US-09-328-352-6912	Sequence 6912, Ap
43	321.5	10.8	442	4	US-09-489-039A-13633	Sequence 13633, A
44	316	10.8	459	4	US-09-489-039A-12384	Sequence 12384, A
45	309	10.4	451	4	US-09-489-039A-7269	Sequence 7269, Ap

ALIGNMENTS

RESULT 1
US-08-647-484-2
Sequence 2, Application US/08647484
Patent No. 5618677
; GENERAL INFORMATION:
; APPLICANT: Ni, Jinhui
; APPLICANT: Paul, Steven M.
; TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
; TITLE OF INVENTION: PHOSPHATE COTRANSPORTER AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,484
; FILING DATE: 14-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,033
; FILING DATE: 27-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-647-484-2

Query Match 100.0%; Score 2970; DB 1; Length 560;
Best Local Similarity 100.0%;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-08-647-481-2
Sequence 2, Application US/08647481
Patent No. 5618918
GENERAL INFORMATION:
; APPLICANT: Ni, Binhui
; APPLICANT: Paul, Steven M.
; TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
; TITLE OF INVENTION: PHOSPHATE COTRANSPORTER AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,481
; FILING DATE: 14-MAY-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,033
; FILING DATE: 27-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-647-481-2

Query Match   100.0%; Score 2970; DB 1; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.8e-278;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-08-430-033A-2
Sequence 2, Application US/0430033A
Patent No. 5686266
GENERAL INFORMATION:
; APPLICANT: Ni, Binhui
; APPLICANT: Paul, Steven M.
; TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
; TITLE OF INVENTION: PHOSPHATE COTRANSPORTER AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:

Qy 181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCCSSYAGAVAVAMPLAGVLVQYSGWSSSVFV 240
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Qy 541 YGATHSTFQPPRPPPPVRDY 560
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Db 541 YGATHSTFQPPRPPPPVRDY 560

Left column

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;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/430,033A
;       FILING DATE:
;       CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Gaylo, Paul J.
;       REGISTRATION NUMBER: 36,808
;       REFERENCE/DOCKET NUMBER: X-10006
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (317) 276-0756
;       TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 560 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-430-033A-2

Query Match      100.0%;  Score 2970;  DB 1;  Length 560;
Best Local Similarity  100.0%;  Pred. No. 1.8e-278;
Matches  560;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
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Right column

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;   APPLICANT: Paul, Steven M.
;   TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
;        PHOSPHATE COTRANSPROTER
;   TITLE OF INVENTION:
;   NUMBER OF SEQUENCES: 3
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Eli Lilly and Company
;       STREET: Lilly Corporate Center
;       CITY: Indianapolis
;       STATE: Indiana
;       COUNTRY: United States of America
;       ZIP: 46285
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: PCT/US96/05792
;       FILING DATE:
;       CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/430,033
;       FILING DATE: April 27, 1995
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Gaylo, Paul J.
;       REGISTRATION NUMBER: 36,808
;       REFERENCE/DOCKET NUMBER: X-10006
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (317) 276-0756
;       TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 560 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;   MOLECULE TYPE: protein
PCT-US96-05792-2

Query Match      100.0%;  Score 2970;  DB 5;  Length 560;
Best Local Similarity  100.0%;  Pred. No. 1.8e-278;
Matches  560;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCPGLP  60
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Qy   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
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Db   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120

Qy  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
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Db  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSSVFYV 240
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Qy  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
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Bottom (left)

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RESULT 4
PCT-US96-05792-2
; Sequence 2, Application PCT/US9605792
; GENERAL INFORMATION:
;   APPLICANT: Ni, Binhui
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Qy  481  GGVIFYGVPASGEKQPWAEPEEMSEEKCCFGVGHDQLAGSDDSEMEDEAEPPGAPPAPPS  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  GGVIFYGVPASGEKQPWAEPEEMSEEKCCFGVGHDQLAGSDDSEMEDEAEPPGAPPAPPS  540

Qy  541  YGATHSTFQPPRPPPPVVRDY  560
         |||||||||||||||||||||
Db  541  YGATHSTFQPPRPPPPVVRDY  560
```

RESULT 5
US-09-949-016-11354
; Sequence 11354, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11354
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11354

Query Match   99.7%; Score 2962; DB 4; Length 567;
Best Local Similarity   99.8%; Pred. No. 1.1e-277;
Matches 559; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy    1  MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    8  MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP   67

Qy   61  RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   68  RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH  127

Qy  121  GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  128  GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG  187

Qy  181  LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  188  LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV  247

Qy  241  YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  248  YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT  307

Qy  301  SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ  360
         ||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||
Db  308  SMPVYAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ  367

Qy  361  IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  368  IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS  427

Qy  421  GFNVNHLDIAPRYASILMGISNGVGTLLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  428  GFNVNHLDIAPRYASILMGISNGVGTLLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY  487

Qy  481  GGVIFYGVPASGEKQPWAEPEEMSEEKCCFGVGHDQLAGSDDSEMEDEAEPPGAPPAPPS  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  GGVIFYGVPASGEKQPWAEPEEMSEEKCCFGVGHDQLAGSDDSEMEDEAEPPGAPPAPPS  540

Qy  541  YGATHSTFQPPRPPPPVVRDY  560
         |||||||||||||||||||||
Db  541  YGATHSTFQPPRPPPPVVRDY  560
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```
Db  488  GGVIFYGVPASGEKQPWAEPEEMSEEKCCFGVGHDQLAGSDDSEMEDEAEPPGAPPAPPS  547

Qy  541  YGATHSTFQPPRPPPPVVRDY  560
         |||||||||||||||||||||
Db  548  YGATHSTFQPPRPPPPVVRDY  567
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RESULT 6
US-08-805-118-4
; Sequence 4, Application US/08805118
; Patent No. 5985604
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
; TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,118
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0221 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 507415
US-08-805-118-4

Query Match   98.5%; Score 2925; DB 2; Length 560;
Best Local Similarity   98.2%; Pred. No. 4.1e-274;
Matches 550; Conservative   5; Mismatches   5; Indels   0; Gaps   0;

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Qy    1  MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP   60
         |||||||||||||||||:|||||||||||||||||||||||||:||||||||||||||||
Db    1  MEFRQEEFRKLAGRALGRLHRLLEKRQEGAETLELSADGRPVTTHTRDPPVVDCTCFGLP   60

Qy   61  RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH  120
         ||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db   61  RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQNWDPETVGLIH   120

Qy  121  GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG  180

Qy  181  LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV  240
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RESULT 7
US-09-391-958-4
Sequence 4, Application US/0391958
Patent No. 6326207
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/391,958
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/805,118
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0221 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 507415
US-09-391-958-4

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Qy  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
        ||||||||||||||||||||||||||||||||||||||||||:||:|||||||||||||
Db  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPVTKFNTPWRRFFT 300

Qy  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
        |||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db  301 SMPVYAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
        |||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 IADFLRSRHIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy  421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy  481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
        |||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db  481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEVEPPGAPPAPPPS 540

Qy  541 YGATHSTFQPPRPPPPVRDY 560
        |||||||:||||||||||||
Db  541 YGATHSTVQPPRPPPPVRDY 560
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Query Match   98.5%;   Score 2925;   DB 3;   Length 560;
Best Local Similarity   98.2%;   Pred. No. 4.1e-274;
Matches 550;   Conservative 5;   Mismatches 5;   Indels 0;   Gaps 0;

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Qy    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTHTRDPPVVDCTCFGLP  60
        ||||||||||||||||||:||:||||||||||||||||||||||:|||||||||||||||
Db    1 MEFRQEEFRKLAGRALGRLHRLLEKRQEGAETLELSADGRPVTTHTRDPPVVDCTCFGLP  60

Qy   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
        |||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFNWDPETVGLIH 120

Qy  121 GSFFWGYIVTQIPGGFICQKFAANRVPGFAIVATSTLNMLIPSAAARVHYGCVIFVRILQG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GSFFWGYIVTQIPGGFICQKFAANRVPGFAIVATSTLNMLIPSAAARVHYGCVIFVRILQG 180

Qy  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSSVPYV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSSVPYV 240

Qy  241 .YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
         |||||||||||||||||||||||||||||||||||||||||:||:|||||||||||||||
Db  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPVTKFNTPWRRFFT 300

Qy  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
        |||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db  301 SMPVYAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
        |||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 IADFLRSRHIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy  421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy  481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
        |||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db  481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEVEPPGAPPAPPPS 540

Qy  541 YGATHSTFQPPRPPPPVRDY 560
        |||||||:||||||||||||
Db  541 YGATHSTVQPPRPPPPVRDY 560
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RESULT 8
US-09-915-181A-5
Sequence 5, Application US/09915181A
Patent No. 6818391
GENERAL INFORMATION:
APPLICANT: EDWARDS, ROBERT
APPLICANT: BELLOCCHIO, ELIZABETH
APPLICANT: FREMEAU, ROBERT
APPLICANT: REIMER, RICHARD
TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS
FILE REFERENCE: 30ST-93261005
CURRENT APPLICATION NUMBER: US/09/915,181A
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/220,556
PRIOR FILING DATE: 2000-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 560
TYPE: PRT
ORGANISM: Rattus rattus
US-09-915-181A-5

Query Match   98.5%;   Score 2925;   DB 4;   Length 560;
Best Local Similarity   98.2%;   Pred. No. 4.1e-274;
Matches 550;   Conservative 5;   Mismatches 5;   Indels 0;   Gaps 0;

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Qy    1 MEFRQEEFRKLAGRALGKIHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP  60
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RESULT 9
US-09-740-041-4
Sequence 4, Application US/09740041
Patent No. 656293
GENERAL INFORMATION:
; APPLICANT: MERKULOV, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001001
; CURRENT APPLICATION NUMBER: US-09/740,041
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 578
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-740-041-4

Query Match   77.9%; Score 2313.5; DB 4; Length 578;
Best Local Similarity   79.3%; Pred. No. 6.3e-215;
Matches   428; Conservative   57; Mismatches   50; Indels   5; Gaps   2;

Qy   1 MEFRQEEFRKLAGRALGRLHRLLEKRQEGAETLELSADGRPVTTHTRDPPVVDCTCFGLP 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MEFRQEEFRKLAGRALGRLHRLLEKRQEGAETLELSADGRPVTTHTRDPPVVDCTCFGLP 60

Qy   61 RXRIIAIMSGLGPCISPGIRCNLGVAIVSMVNNSTTHRGGHVVQKAQFSWDPETVGLIH 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RXRIIAIMSGLGPCISPGIRCNLGVAIVSMVNNSTTHRGGHVVQKAQFSWDPETVGLIH 120

Qy   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCCSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCCSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300

Qy   301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 SMPVYAIIVANFCRSWTFYLLLISQPAYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy   361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 IADFLRSRHIMSTTNVRKLMNCCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy   421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDESEMEDEVEPPGAPPAPPPS 540

Qy   541 YGATHSTFQPPRPPPPPVRDY 560
            |||||||||||||||||||||
Db   541 YGATHSTVQPPRPPPVRDY 560

RESULT 10
US-09-915-181A-4
Sequence 4, Application US/09915181A
Patent No. 6818391
GENERAL INFORMATION:
; APPLICANT: EDWARDS, ROBERT
; APPLICANT: BELLOCCHIO, ELIZABETH
; APPLICANT: REIMER, ROBERT
; APPLICANT: FREMEAU, RICHARD
; TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS
; FILE REFERENCE: 3057-93261OUS
; CURRENT APPLICATION NUMBER: US/09/915,181A
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/220,556
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-915-181A-4

Query Match   77.9%; Score 2313.5; DB 4; Length 582;
Best Local Similarity   79.3%; Pred. No. 6.4e-215;
Matches   428; Conservative   57; Mismatches   50; Indels   5; Gaps   2;

Db   132 WGYIITQIPGGYIASRLAANRVFGFAAILLTSTLNMLIPSAARVHYGCVIFVRILQGLVEG 191
            ||||||||:||| :::   :: :||||
Qy   125 WGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEG 184

Db   192 VTYPACHGIWSKWAPPLERSRLATTAFCCSYAGAVIAMPLAGVLVQYSGWSSSVFVYVYGSF 251
            |||||||||||||||||||||||||||||||||||||:|||||||:|:|
Qy   185 VTYPACHGIWSKWAPPLERSRLATTAFCCSYAGAVVAMPLAGVLVQYSGWSSVFYVYGSF 244

Db   252 GMVWMFWLLLVSYESPAKIPTITDBERRYIEESIGESANLLGAMEKFKTPWRKFFTSMPV 311
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   245 GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPV 304

Db   312 YAIIVANFCRSWTFYLLLISQPAYFEEVGFEISKVGMLSAVPHLVMTIIVPIGQIADF 371
            |||||||||||||||||||||||||||||||||||||:||::||||||||||||
Qy   305 YAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQIADF 364

Db   372 LRSKQILLSTTTVRKLMNCGGFGMEATLLLVVGYSHTRGVAISFLVLAVGFSGFAISGFNV 431
            |||||||||||||||||||||||||||||||||||||:||||:|||||||||||||||||
Qy   365 LRSRRIMSTTNVRKLMNCCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGFNV 424

Db   432 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKQKSREENQYVFLIAALVHYGGVI 491
            ||||||||||||||||||||||||||||||||||||:|:||||||||||||:||||||||
Qy   425 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVI 484

Db   492 FYALFASGEKQPWADPEEETSEEKCGFIHEDEL-----DEETGDIIQ-NYINYGTTKSYGAT 546
            |:||:|||||||||| :|::: || :||||:|| :| | ||||
Qy   485 FYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPSYGAT 544

Qy   245 GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPV 304

```
Qy   253  GMVWTMFWLLVSYESPAKHPTITDEERRYIEESIGESANLLGAMEKFKTPWRKFFTSMPV  312
Db        YAIIVANFCRSWTFYLLLISQPDYEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADF  (Qy 305-364)
Db   313  YAIIVANFCRSWTFYLLLISQPAYFEEVFGFAISKVGMLSAVPHLVMTIIVPIGGQIADF  372
Qy   365  LRSRRIMSTTNVRKLMNCGGFGMEATLLLLVVGYSHSKGVAISFLVLAVGFSGFAISGFNV  424
Db   373  LRSRQILSTTTVRKIMNCGGGFGMEATLLLLVVGYSHTRGVAISFLVLAVGFSGFAISGFNV  432
Qy   425  NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQVFFLIASLVHYGGVI  484
Db   433  NHLDIAPRYASILMGISNGVGTLSGMYCPIIVGAMTKNKSREEWQVFFLIAALVHYGGVI  492
Qy   485  FYGVFASGEKQPWAEPEEMSEEKCCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPSYGAT  544
Db   493  FYALFASGEKQPWADPEETSEKCCGFIHEDEL---DEETGDITQ-NYINYGTTKSYGAT  547
```

RESULT 11
US-09-740-041-2
; Sequence 2, Application US/09740041
; Patent No. 652593
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001001
; CURRENT APPLICATION NUMBER: US/09/740,041
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Human
US-09-740-041-2

Query Match   73.6%; Score 2185; DB 4; Length 589;
Best Local Similarity   76.3%; Pred. No. 1.8e-202;
Matches   412; Conservative   53; Mismatches   69; Indels   6; Gaps   3;

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Qy     5  QEBFRKLAGRALGKLHRLLEKRQEGEAETLELSADGRPVTTQTRDPPVVDCTCFGLPRRYI   64
Db    18  KEGVKNAVGDSLGILQRKIDGTTEEEDNIELNEEGRPVQTSRSPPLCDHCCGLPKRYI    77
Qy    65  IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGHVVVQKAQFSWDPETVGLIHGSFF  124
Db    78  IAIMSGLGFCISFGIRCNLGVAIVEMVNNSTVYVDGKPEIQTAQFNWDPETVGLIHGSFF  137
Qy   125  WGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEG  184
Db   138  WGYIMTQIPGGFISNKFAANRVFGAAIFLTSTLNMFIPSAARVHYGCVMCVRILQGLVEG  197
Qy   185  VTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYYYGSF  244
Db   198  VTYPACHGMWSKWAPPLERSRLATTSFCGSYAGAVVAMPLAGVLVQYIGWASAPYI    257
Qy   245  GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPV  304
Db   258  GIIWYMFWLLQAYECPAAHPTISNEEKTYIETSIGEGANVVS-LSKFSTPWKRFFTSLPV  316
Qy   305  YAIIVANFCRSWTFYLLLISQPDYEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADF  364
Db   317  YAIIVANFCRSWTFYLLLISQPAYFEEVFGFAISKVGLLSAVPHMVMTIIVPIGGQIADY  376
Qy   365  LRSRRIMSTTNVRKLMNCGGFGMEATLLLLVVGYSHSKGVAISFLVLAVGFSGFAISGFNV  424
Db   377  LRSRQILTTTAVRKIMNCGGGFGMEATLLLLVVGFSHTRGVAISFLVLAVGFSGFAISGFNV  436
Qy   425  NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQVFFLIASLVHYGGVI  484
Db   437  NHLDIAPRYASILMGISNGVGTLSGMYCPIIVGAMTRHKTREEWQVFFLIAALVHYGGVI  496
Qy   485  FYGVFASGEKQPWAEPEEMSEEKCCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPSYGAT  544
Db   497  FYGVFASGEKQPWADPENLSEEKCGIIDQDELA--EEIELNHES---FASPKKKMSYGAT  551
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RESULT 12
US-09-915-181A-3
; Sequence 3, Application US/0991518lA
; Patent No. 6818391
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ROBERT
; APPLICANT: BELLOCCHIO, ELIZABETH
; APPLICANT: FREMEAU, ROBERT
; APPLICANT: REIMER, RICHARD
; TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS
; FILE REFERENCE: 305T-93261OUS
; CURRENT APPLICATION NUMBER: US/09/915,181A
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/220,556
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 850
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-181A-3

Query Match   73.2%; Score 2174.5; DB 4; Length 850;
Best Local Similarity   76.0%; Pred. No. 3.2e-201;
Matches   414; Conservative   51; Mismatches   69; Indels   11; Gaps   5;

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Qy     5  QEBFRKLAGRALGKLHRLLEKRQEGEAETLELSADGRPVTTQTRDPPVVDCTCFGLPRRYI   64
Db    26  KEGVKNAVGDSLGILQRKLDGTNEEGDAIELSEEGRPVQTSRARAPVCDCSCCGIPKRYI   85
Qy    65  IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGHVVVQKAQFSWDPETVG----LIH  120
Db    86  IAVMSGLGFCISFGIRCNLGVAIVEMVNNSTVYVDGKPEIQTAQFNWDPETVGVRANSLIH  145
Qy   121  GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG  180
Db   146  GSFFWGYIVTQIPGGFISNKFAANRVFGAAIFLTSTLNMFIPSAARVHYGCVMCVRILQG  205
Qy   181  LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV  240
Db   206  LVEGVTYPACHGMWSKWAPPLERSRLATTSFCGSYAGAVVAMPLAGVLVQYIGWASAPYI  265
Qy   241  YGSFGIFWYLFWLLV-SYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFF  299
Db   266  YGMFGIIWYMFWLLQAYECPAVHPTISNEEKTYIETSIGEGANLAS-LSKFNTPWKRFF  324
Qy   300  TSMPVYAIIVANFCRSWTFYLLLISQPDYEEVFGFEISKVGLVSALPHLVMTIIVPIGG  359
Db   325  TSLPVYAIIVANFCRSWTFYLLLISQPAYFEEVFGFAISKVGLLSAVPHMVMTIIVPIGG  384
Qy   360  QIADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLLVVGYSHSKGVAISFLVLAVGFSGFAI  419
Db   385  QIADYLRSRKILTTTAVRKIMNCGGGFGMEATLLLLVVGFSHTKGVAISFLVLAVGFSGFAI  444
Qy   420  SGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQVFFLIASLVH  479
Db   445  SGFNVNHLDIAPRYASILMGISNGVGTLSGMYCPIIVGAMTRHKTREEWQVFFLIAALVH  504
Qy   480  YGGVIFYGVFASGEKQPWAEPEEMSEEKCCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPP  539
Db   505  YGGVIFYGVFASGEKQPWADPENLSEEKCGIIDQDELA--EETELNHEA---FVSPRKKM  559
Qy   540  SYGAT  544
Db   560  SYGAT  564
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RESULT 13
US-08-864-785-1
Sequence 1, Application US/08864785A
Patent No. 6329566
GENERAL INFORMATION:
APPLICANT: Kaplan, Joshua M.
APPLICANT: Oppenheimer, Allison J.
APPLICANT: Hart, Anne C.
TITLE OF INVENTION: METHODS FOR THE DETECTION, TREATMENT, AND PREVENTION OF NEURODEGENERATION
FILE REFERENCE: 00786/353001
CURRENT APPLICATION NUMBER: US/08/864,785A
CURRENT FILING DATE: 1997-05-29
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-08-864-785-1

Query Match   43.7%;   Score 1297;   DB 3;   Length 576;
Best Local Similarity 47.7%;   Pred. No. 1.4e-116;
Matches 262;   Conservative 88;   Mismatches 171;   Indels 28;   Gaps 10;

```
Qy    9 RKLAGRALGKLHRILEKRQEBGAEFLELSADGRPVTTQTRDP---PVVDCTCFGLPR-RYI 64
          :::   ||||  ||  |||| :|  |||  ||  | |:| || :|:
Db   12 KQMWGEPLAKMTAAAASATGAAPPQOMQEEGNENPMQMHSNKVLQVMEQTWIGKCKRKWL 71

Qy   65 IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFF 124
          :||: ||||||||||||:||   |:||: :||   |:|:|| :::||:|||
Db   72 LAILANMGFMISFGIRCNFGAAAKTHMYKNYTDPYG---KVHMHEFNWTIDELSVMESSYF 128

Qy  125 WGYIVTQIPGFGFICQKFAANRVRFGFAIVATSTLNMLIPSAARVHYG-CVIFVRILQGLVE 183
         :||:|||||.||:|.||.|||:|||||:|.|||||||:||||||:.||  :|  | |:||:
Db  129 YGYLVTQIPAGFLAAKFPPNKLFGFGIGVGAFLNILLPYGFKVKSDYLVAFIQITQGLVQ 188

Qy  184 GVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYVYGS 243
         || |||:||:|..|||::||:|||||||.||||||.. |:| ||:.||:.|:: |||||:
Db  189 GVCYPAMHGVWRYWAPPMERSKLATTAFTGSYAGAVGLPLSAFLVSYSVSWAAPFYLYGV 248

Qy  244 FGIFWYLFWLLVSYESPSPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMP 303
          | :| :||.|..:|::| |||||:||||:::||||||| :||| |  :.:|||:| | :
Db  249 CGVIWAILWFCVTFEKPAPHPTISQEEKIFIEDAIGHVSN-THPTIR-SIPWKAIVTSKP 306

Qy  304 VYAIIVANFCRSWTFYILLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIAD 363
         |:||||||| ||||||:||| .|  .|: ||| || .|||.|||||||  :|:|||| ||
Db  307 VWAIIVANFARSWTFYLLLLQNQLTYMKEALGMKIADSGLLAAIPHLVMGCVVLMGGQLAD 366

Qy  364 FLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFPAISGFN 423
          |||:::||||||.|| |||||.: ||::|:|  :.|. .| : ::||.||.|||||||||
Db  367 YLRSNKILSTTAVRKIFNCGGFGGBEAAFMLIVAYTTSDTTAIMALIAAVGMGGFAISGFN 426

Qy  424 VNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYFLIASLVHYGGV 483
         ||||||||||:|||||.|||.||| || .||:.|: :|  |: |.|  |||||.|: ||
Db  427 VNHLDIAPRYAAILMGFSNGIGTLAGLTCPFVTEAFTAH-SKHGWTSVFLLASLIHFTGV 485

Qy  484 IFYGVFASGEKQPWAEPEEMSE------EKCGFVG--------HDQLAGSDDSEMEDE 527
          || :.|||| | |||| ::      :||  |            |:|| || |  |
Db  486 TFYAVYASGELQEWAEPKEEEWSNKELVNKTGINGTGYGAAEFTFTQLPAGVDSSYQAQ 545

Qy  528 AEP-PGAPP 535
         | | || :|
Db  546 AAPAPGTNP 554
```

RESULT 14
US-09-915-181A-6
Sequence 6, Application US/09915181A
Patent No. 6818391
GENERAL INFORMATION:

APPLICANT: EDWARDS, ROBERT
APPLICANT: BELLOCCHIO, ELIZABETH
APPLICANT: FREMEAU, ROBERT
APPLICANT: REIMER, RICHARD
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS
FILE REFERENCE: 3057-93261OUS
CURRENT FILING DATE:
CURRENT APPLICATION NUMBER: US/09/915,181A
PRIOR APPLICATION NUMBER: US 60/220,556
PRIOR FILING DATE: 2000-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
; LENGTH: 563
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-915-181A-6

Query Match   43.6%;   Score 1294;   DB 4;   Length 563;
Best Local Similarity 47.9%;   Pred. No. 2.7e-116;
Matches 262;   Conservative 86;   Mismatches 171;   Indels 28;   Gaps 10;

```
Qy   11 LAGRALGKLHRILEKRQEBGAEFLELSADGRPVTTQTRDP---PVVDCTCFGLPR-RYIIA 66
         |   ||||  ||  |||| :|  |||  ||  | |:| || :|:        :|: ||
Db    1 MVGEPLAKMTAAAASATGAAPPQOMQEEGNENPMQMHSNKVLQVMEQTWIGKCKRKWLLA 60

Qy   67 IMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFFWG 126
         :||| ||||||||||:||   |:||: :||   |:|:|| :::||:|||       ||:|
Db   61 ILANNGFMISFGIRCNFGAAKTHMYKNYIDPYG---KVHMHEFNWTIDELSVMESSYFYG 117

Qy  127 YIVTQIPGGFICQKFAANRVRFGFAIVATSTLNMLIPSAARVHYG-CVIFVRILQGLVEGV 185
         |:|||||.||:|.||.|||:|||||:|.|||||||:||||||:.||  :|  | |:||:||
Db  118 YLVTQIPAGFLAAKPPNKLFGFGIGVGAFLNILLPYGFKVKSDYLVAFIQITQGLVQGV 177

Qy  186 TYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYVYGSFG 245
         .|||:||:|..|||::||:|||||||.||||||.. |:| ||:.||:.|:: |||||:.|
Db  178 CYPAMHGVWRYWAPPMERSKLATTAFTGSYAGAVGLPLSAFLVSYSVSWAAPFYLYGVCG 237

Qy  246 IFWYLFWLLVSYESPSPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPVY 305
         :| :| :||.|..:|::| |||||:||||:::||||||| :||| |  :.:|||:| | :|
Db  238 VIWAILWFCVTFEKPAPHPTISQEEKIFIEDAIGHVSN-THPTIR-SIPWKAIVTSKPVW 295

Qy  306 AIIVANFCRSWTFYILLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADFL 365
         ||||||| ||||||:||| .|  .|: ||| || .|||.|||||||  :|:|||| ||:|
Db  296 AIIVANFARSWTFYLLLLQNQLTYMKEALGMKIADSGLLAAIPHLVMGCVVLMGGQLADYL 355

Qy  366 RSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFPAISGFNVN 425
         ||:::||||||.|| |||||.: ||::|:|  :.|. .| : ::||.||.|||||||||||
Db  356 RSNKILSTTAVRKIFNCGGFGGBEAAFMLIVAYTTSDTTAIMALIAAVGMGGFAISGFNVN 415

Qy  426 HLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYFLIASLVHYGGVIF 485
         |||||||:|||||.|||.||| || .||:.|: :|  |: |.|  |||||.|: ||:|
Db  416 HLDIAPRYAAILMGFSNGIGTLAGLTCPFVTEAFTAH-SKHGWTSVFLLASLIHFTGVTF 474

Qy  486 YGVFASGEKQPWAEPEEMSE------EKCGFVG--------HDQLAGSDDSEMEDEAE 529
         |.|||| | |||| ::      :||  |            |:|| || |  |   |
Db  475 YAVYASGELQEWAEPKEEEWSNKELVNKTGINGTGYGAAEFTFTQLPAGVDSSYQAQAA 534

Qy  530 P-PGAPP 535
         | || :|
Db  535 PAPGTNP 541
```

RESULT 15
US-09-359-167-2
Sequence 2, Application US/09359167
Patent No. 6803448
GENERAL INFORMATION:
APPLICANT: Hellerqvist, Carl
APPLICANT: Fu, Changlin
TITLE OF INVENTION: GBS Toxin Receptor
FILE REFERENCE: CARB-008/01US
CURRENT APPLICATION NUMBER: US/09/359,167

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;  CURRENT FILING DATE: 1999-07-21
;  EARLIER APPLICATION NUMBER: 60-693,843
;  EARLIER FILING DATE: 1998-07-22
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: Patentin Ver. 2.0
;  SEQ ID NO 2
;  LENGTH: 495
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-09-359-167-2

Query Match          31.6%;  Score 940;  DB 4;  Length 495;
Best Local Similarity    39.5%;  Pred. No. 4e-82;
Matches 193;  Conservative  93;  Mismatches 162;  Indels  40;  Gaps   8;

Qy     38  DGRPVTTQTRDPPVVDCTCFGLPR------------------RYIIAIMSGLGFCISFGTRCNLGVAI  87
               :  ;      :|.:                           ||:||:||:|:|||.|::
Db     12  DGEESTDRT---PLLP----GAPRAEAAPVCCSARYNLAILAPFGFPIVYALRVNLSVAL  64

Qy     88  VSMVNNSTT---------HRGGHVVVQKAQ----FSWDPETVGLLIHGSFFWGYIVTQI  132
               |:|:|:||         |||||     ||||   :|::::||:||::||::|:||.||
Db     65  VDMVDSNTTLEDNRTSKACPEHSAPIKVHHNQTGKKYQWDAETQGWILGSFFYGYIITQI  124

Qy    133  PGGFICQKFAANRVFGPAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEGVTYPACHG  192
               :|| |:: |.:   |.::|||||||:||  :|:  :|::|:|::|||||:|| ||:|
Db    125  PGGYVASKIGGKMLLGFGILGTAVLILFTPIAADLGVGPLIVLRALEGLGEGVTFPAMHA  184

Qy    193  IWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVVFYVYGSFGIFWYLFW  252
               :||  ||||||:|  |.:|| .|||:::|::|||:|:.|||.||||:|:::||| |||||| |||
Db    185  MWSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYMWMTYVFFPRGTIGIFWFLLW  244

Qy    253  LLVSYESPALHPSISEEERKYIEDALGESAKLMNPL-TKFSTPWRRFFTSMPVYAIIVAN  311
               .: .::|  |.:  ||:|:|:|||||.:||:|:|  ||::||:::|.:.||:|::|::
Db    245  IWLVSDTPQKHRISHYEKEYI-----LSSIRNQLSSQKSVPWVPILKSLPLMAIVVAH  298

Qy    312  FCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADFLRSRRIM  371
               |||||.||||.|:||.|::.:|: |::|||.:||:||||:|:.|.|||.||||||.|||
Db    299  FSYNWTFYTLITLLPTYMKEIIRFNVQENGFLSSLPYLGSWLCMILSGQAADNLRAXWNP  358

Qy    372  STTNVRKLMNCGGFGMEATLLLVVGY-SHSKGVAISFLVLAVGFSGFAISGFNVNHLDIA  430
               ||:|| :|:||.||:||.|::.||||  ||:||||.||:.||:.||:|||.|:|||:|||
Db    359  STLCVRIFSLIGMIGPAVFLVAAGFIGCDYSLAVAFLTISTTLLGGFCSSGFSINHLDIA  418

Qy    431  PRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVIPYGVFA  490
               |||||::||:||:||:|||| ||:|| | ::||:|||:.|:||:.|||:||||:|:|.||
Db    419  PSYAGILLGITNTPATIPGMVGPVIAKSLTPDNTVGEWQTVFYIAAAINVFGAIFFTLPA  478

Qy    491  SGEKQPWA  498
               ||:| ||
Db    479  KGEVQNWA  486
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Search completed: June 2, 2005, 11:32:55
Job time : 27 secs

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: June 2, 2005, 11:28:43 ; Search time 56 Seconds
                 (without alignments)
                 1150.617 Million cell updates/sec

Title: US-10-734-731-4
Perfect score: 2970
Sequence: 1 MEFRQEEFRKLAGRALGKLH.........YGATHSTFQPPRPPPPVRDY 560

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 546557 seqs, 115061664 residues

Total number of hits satisfying chosen parameters: 546557

Maximum DB seq length: 200000000
Minimum DB seq length: 0

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Pending_Patents_AA New:*
                 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
                 2: /cgn2_6/ptodata/2/paa/US05_NEW_COMB.pep:*
                 3: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
                 4: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
                 5: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
                 6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
                 7: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
                 8: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*
                 9: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	1198.5	560	7	US-11-097-143-4995	Sequence 4995, Ap
2	986.5	502	7	US-11-097-143-8367	Sequence 8367, A
3	986.5	502	7	US-11-097-143-24411	Sequence 24411, A
4	927	460	8	US-60-655-875-146571	Sequence 146571,
5	798	559	7	US-11-097-143-2895	Sequence 2895, Ap
6	769.5	516	7	US-11-097-143-27831	Sequence 27831, A
7	767.5	529	7	US-11-097-143-17844	Sequence 17844, A
8	747	493	7	US-11-097-143-5532	Sequence 5532, Ap
9	726	477	8	US-60-669-241-29729	Sequence 29729, A
10	719.5	496	7	US-11-097-143-11013	Sequence 11013, A
11	716.5	465	7	US-11-097-143-20922	Sequence 20922, A
12	708	465	8	US-60-669-175-21828	Sequence 21828, A
13	699.5	475	7	US-11-097-143-28257	Sequence 28257, A
14	699.5	491	7	US-11-097-143-37224	Sequence 37224, A
15	698.5	512	7	US-11-097-143-9567	Sequence 9567, Ap
16	695.5	524	7	US-11-097-143-21597	Sequence 21597, A
17	693.5	479	7	US-11-097-143-15315	Sequence 15315, A
18	692	478	8	US-60-669-175-22572	Sequence 22572, A
19	685.5	497	7	US-11-097-143-37218	Sequence 37218, A
20	676	462	7	US-11-097-143-37221	Sequence 37221, A
21	671	481	7	US-11-097-143-19404	Sequence 19404, A
22	644.5	792	7	US-11-097-143-6948	Sequence 6948, Ap
23	616	465	1	PCT-US05-11532-1919	Sequence 1919, Ap
24	616	465	1	PCT-US05-11532-1920	Sequence 1920, Ap
25	615	495	7	US-11-097-143-20859	Sequence 20859, A
26	596.5	449	7	US-11-097-143-2769	Sequence 2769, Ap
27	595.5	313	8	US-60-669-175-28254	Sequence 28254, Ap
28	577	468	7	US-11-097-143-17484	Sequence 17484, A
29	558	444	7	US-11-097-143-20862	Sequence 20862, A
30	557	492	7	US-11-097-143-3039	Sequence 3039, Ap
31	496	473	7	US-11-097-143-6987	Sequence 6987, Ap
32	483	401	6	US-11-936-061-113	Sequence 113, App
33	483	401	6	US-10-936-626-113	Sequence 113, App
34	481	379	6	US-10-533-176-18	Sequence 18, Appl
35	477	420	6	US-10-936-061-112	Sequence 112, App
36	477	420	6	US-10-936-626-112	Sequence 112, App
37	469.5	452	8	US-60-669-175-23389	Sequence 23389, A
38	468.5	307	6	US-10-450-763-43033	Sequence 43033, A
39	434	614	6	US-10-450-763-52551	Sequence 52551, A
40	433	246	8	US-60-669-175-35181	Sequence 35181, A
41	433	287	8	US-60-669-175-21944	Sequence 21944, A
42	426.5	309	7	US-11-097-143-27828	Sequence 27828, A
43	415.5	439	7	US-11-097-143-38628	Sequence 38628, A
44	412	247	8	US-60-669-241-27469	Sequence 27469, A
45	386.5	438	7	US-11-043-889-55	Sequence 55, Appl

ALIGNMENTS

RESULT 1
US-11-097-143-4995

Sequence 4995, Application US/1109714

; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 4995
; LENGTH: 560
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-4995

Query Match   40.4%; Score 1198.5; DB 7; Length 560;
Best Local Similarity   46.8%; Pred. No. 5.2e-88;
Matches 244; Conservative 70; Mismatches 144; Indels 63; Gaps 11;

Qy   38 DGRPVT-----TQPRDPPV-------VDCTCFGLPRRYIIAIMSGLGFCISFGTRCNLGV 85
            ||| ||||| |:||:||:::::||||:|.||||:|.||: |||||
Db   61 DDRPDSPASFEIERPLPRKIDKYCKABCPC--MPARYTIATMACVGFMIAFGMRCNMSA 118

Qy   86 AIVSMVANSTTHRGGHVVVQKAQFSWDPETVGLIHGSFFWGYIVTQIPGGFICQXFAANR 145
            ||:||:::|||:|:::::||::|:::|:::::||::|:||||||:||||:|:|::||
Db   119 AKLKGEHNGTVF-------------MNWTVAVESHVDSSFFWGYLVTQIPGGFIASKFPANK 167

RESULT 2
US-11-097-143-8367
Sequence 8367, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8367
; LENGTH: 502
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-8367

Query Match   33.2%; Score 986.5; DB 7; Length 502;
Best Local Similarity   38.0%; Pred. No. 4.8e-71;
Matches 200; Conservative 96; Mismatches 185; Indels 45; Gaps 7;

Qy   146 VFGFAIVATSTLNMLIPSAARVHYG-CVIFVRLLQGLVEGVTYPACHGIWSKWAPPLERS 204
                | ||: |:: | ::|::||:| |:::|||:|:: | |: | || ||||||:
Db   168 IFGLSIVSSATLHLFVPFAMTLMHGHVVICVRVLQGLFEGVTYPACHGIWRFWAPPMERS 227

Qy   205 RLATTAFCCGSYAGAVVAMPLAGVLVQYSGWSSVSFYVYGSFGIWYTLFWLLVSYESPALHP 264
                |||| | |||:|||:||| ||| ::| | | :|||:| |||:|:|:|| ::|:|||||
Db   228 RLATIAFSGGSYAGVVVGLPLSGLLADAVGYQAPYAYGVFGIIWMFWLCFENPRKHP 287

Qy   265 SISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPVYAIIVANCRSWTFYLLLIS 324
                |||||:||||| | | :: | ||| ||::| ||:::| ||| ||:|||:|||||||
Db   288 AISIPELKYIEKSLGESAIPTMPSLK-TIPWREMMRSMPVYAIIVANFCRSWNYILVLF 346

Qy   325 QPDYFEEVFGFEISKVGLIVSALPHLVMTIIVPIGGQIADFLRSRRIMSTTNVRKLMNCGG 384
                ||||:|| ||:|||||||:|||:|||| |:| :||||| |||::|:|:||||:|||:|||
Db   347 QSSFLKHKFGFKYEEAGFVGSLPHLIMTIIVPEGGMLADHLRKNGILSTTNVRKLFNCGG 406

Qy   385 FGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGENVNNHLDIAPRYASILMGISNGV 444
                ||| :|||: |:|| | |:|:: |||| ||||:|:||:|||||| ||||| ||:|||:
Db   407 FGMEGLPFLFVAHSSTATGAMFALTCGVAFSGFAISGYNVNHLDIAPRYASILMGLSNGI 466

Qy   445 GTLLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVIFYGVFASGEKQPWAEPEEMS 504
                | || |:|||||||| |||||||||:|||||:|||||||||||:|||| : | :
Db   467 GTLAGIIVP---------------------------YALDGLIQANGAPEY---------- 497

Qy   505 EEKC---GFVGHGDLAGSDDSEMEDEAEPPGAPPAPPPSYG 542
                       | || ||| | | | | |: | |:
Db   498 QSTAISYGATGH---VANNPFAMASGA-PPIAEEDAPPYG 534

RESULT 3
US-11-097-143-24411
Sequence 24411, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24411
; LENGTH: 502
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-24411

Query Match   33.2%; Score 986.5; DB 7; Length 502;
Best Local Similarity   38.0%; Pred. No. 4.8e-71;
Matches 200; Conservative 96; Mismatches 185; Indels 45; Gaps 7;

Qy   73 FCISFGIRCNLGVAIVSMNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFFWGIVTQI 132
                | :: | | |||:| :| | ||:|: |||:| |: | | ||:|:|||| | ||:
Db   49 FFNVYSLRVNLSVAIVAMTENRTVFDADGNVSYQQDFPWDSKQKGLILSSFFYGIVTQF 108

Qy   133 PGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRLLQGLVEGVTYPACHG 192
                || :| |||::|:|||||||||||||| ||||||||| ||:||||||:|||||||||||
Db   109 LGGYIGTKIGGNIVFGTGIGSSTAILTLLTPMAASHSLEMFLFVRLIIEGFFEGVTPGIHA 168

Qy   193 IWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVSFYVYGSFGIWYLFW 252
                ||||||||:| ||||| | ||||||| ||||||||:||| | | :|||:|||| |: |
Db   169 VWARWSPPLERSRMASIAFAGNYAGTVVAMPCCSGFLATKYGWESVFYVGTIGVTWITW 228

Qy   253 LLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPVYAIIVANF 312
                |||||||||||| ||||:|||||| | | :: | ||| ||::| ||:::| |||||||
Db   229 LVFVKAGPELDRFCSKEECDYIQKTIGYYGS-----KHVRGHPWRAIFTSMPPYAIMASHF 283

Qy   313 CRSWTFYLLLISQPDYFEEVFGFEISKVGLIVSALPHLVMTIIVPIGGQIADFLRSRRIMS 372
                |||:|||| ||| ||||:|| ||:||||||:|||:|||| |:|::||||| |||::|:|
Db   284 SENWGFYTLLITQLPSFLRDTLNFDLGKTGILSAVPYLAMGILLAVSGYLADWLQVKGIWT 343

Qy   373 TTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGENVNNHLDIAPR 432
                |||:|||:||||||| :||| ||:|| | |:|: |||||| ||||:|:|| ||||||
Db   344 TTQVRRNFNCGAFLAQTVFMMLTAYLLDPWSVVSLTIAVGLGFAPAWSGFAVNHLDIAPQ 403

Qy   433 YASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVIFYGVFASG 492
                ||||||| |||| |: |:|||||||| |||||||||||:|||||:||:|||||||:|||
Db   404 HASVLMGIGNTFATIPGIVSPLLTGYVVTINQTSDEWRIIFISAGIYLVGCVIYWFYCSG 463

Qy   493 EKQPWAE-PEEMSEE----------KCCGFVGHGDLAGSDDSEMED 526
                :|||||: |: | || ||| | |
Db   464 DLQEWAKTPEQKAQEAEEEKAQLQLTQTAGFV--------NSGAELKO 502

```
Qy     13  GRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDDPVVDCTCFGLPRRYIIAIMSGLG    72
               ||:   |:|
Db     10  GKHLEQVH----------QNNEITE----SEPLTWR----------FWRKQRYIVVLLAFFG    48

Qy     73  FCISFGLTRCNLGVAIVSMVNNSTTHRGGHVVVQKAQPSWDPETVGLIHGSFPWGYIVTQI   132
            ||:|: |||||||||||||||:|||||||||||:||||||::|||
Db     49  FPNVVSLRVLNSVAIVAMTENRTVFPADGNVSYQQDPPWDSKQKGLILSSFFYGYILTQF   108

Qy    133  PGGFICQKPAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILCQLVEGVTYPACHG   192
                  :|:|:||||||||:|:||
Db    109  LGGYIGTKIGGNIVFGTGIGSTAILLILTPWAASHSLEMFLPVRIIEGFPEGVTPGIHA   168

Qy    193  IWSKWAPPLERSRLATTAFCCSSYAGAVVAMPLLAGVLVQYSGWSSVSFYYYGSPGIFWYLFW   252
            |:|:||||||||||||||:|::::|:||||||||||||:||:||:||:::|
Db    169  VWAARWSPPLERSRMASIAFAGNYAGTVVAMPCSGFLATKYGWESVFVVPGTIGVIWYITW   228

Qy    253  LLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPVYAIIVANF   312
            ||  ||||||||||||||:||||||||||||:||:|::||:||||::||||:||
Db    229  LVFVKAGPELDRFCSKEECDIIQKIIGYVGS----KHVKIPWRAIFTSMPFYAIMASHF   283

Qy    313  CRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADFLRSRRIMS   372
            |:||||||||||||||||||||||||||||||||||||||||||||||:|||||:
Db    284  SENWGFYTLLTQLPSFLRDTLNFDLGKTGILSAVPVLAMGILLAVSGYLADWLQVRGIWT   343

Qy    373  TTNVRKLMNCGGFGMEATLLLLVVGYSHSKGYAISFLVLAVGFSGFAISGFNNVHLIDIAPR   432
            :|||||||||||       :|||||||||||||||||||||||:||
Db    344  TTQVRNFNCGAFLAQTVFVMMLTAYLLDPTWSVVSLTIAVGLGAFAWSGFAVNHLIDIAPQ   403

Qy    433  YASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVIFYGVFASG   492
                |||:|||||||||||||:|||||:|::|||||||||||||||:|||:|
Db    404  HASVLMGIGNTFATIPGIVSPLLTGVVVTNQTSDEWRIIFISAGIYLVGCVIYWFYCSG   463

Qy    493  EKQPWAE-PEEMSEE------------------KCGFVGHDQLAGSDDSEMED    526
            ||:|                         |:|:
Db    464  DLQEWAKTPEQKAQEAEEKAQLIQTAGFV---------NSGAELKD        502
```

Query Match   31.2%;   Score 927;   DB 8;   Length 460;

```
Qy    172  VIFVRILCQLVEGVTYPACHG-------------------------------IWSKWAPPLERSRLATTAF   211
            :|||:||||||||||||||||                           |||||||||||||||||
Db     10  VALVQIAGQLVQGLAYPAMHGGLVQGLAYPAMHGGLVCHWAPVWNCHWAPPLERSKLATTAF    69

Qy    212  CG-------SYAGAVVAMPLAGVLVQYSGW----------------SSVFYVYGSPGIFWYLFWLLVS   256
                   ||||||||||||||||:|||                  ::|:|:||:||||:|| ::
Db     70  TGSSYAGAVFGLSYAGAVPGLPLSALLVSYVHVHSMPFYISMPFYIYGVAGVIWSVFWFSMT   129

Qy    257  YESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPVYAIIVANFCRSW   316
            ||||||||||||||||||||||||   |:|:::|:|||:::|::||||||||||:
Db    130  FEKPAFHPTITVQBKQITEAQIG-PVNQSHPTVR-TIPWRAILTSKPVWAIIVANFARSW   187

Qy    317  TFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADFLRSRRIMSTTNV   376
            |||||||||||||||||||||||||||||||||:|||||||||||||||||:|||||
Db    188  NFYLLLQNQLTYMRDVLGLRISDSGLIAALPHAVMGCVLLIGGRLADYLRSNKILSTPAV   247

Qy    377  RKLMNCGG----------FGMEATLLLLVVGYSHSKGYAISFLVLAVGFSGFAISG------   421
            |||:|||         :|||||||||||||||||||||||||||||||||||:
Db    248  RKLFNCGGFGCGEAFGCEALPLLFVAYTKSERTAMIAFIFHFIPSGFAISGFNNVHLIDIAP   307

Qy    422  ------FNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIA   475
                  |||||||||  ::|||||||||||||||||||:||||||:|::|||||||||||:
Db    308  RYAAILFNVNHLDIAPRYAAILMGFSNGIGTLAGLTCPFVVESLTS-RNANGWVTVFLLA   366

Qy    476  SLVHYGGVIFYGVFAASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEALEPPGAPP   535
            |||:||||:||||||:||:||||| :|:             ::||:||||:||
Db    367  SLIHFTGITFYAYVASGELQEWAEPKPNEEE---------------SSTDFHQSTAQNONGTA   415

Qy    536  APPP----SYGATHST    547
            ||||    :||::|:|
Db    416  ATNPFMPIGATTFT    429
```

Query Match   26.9%;   Score 798;   DB 7;   Length 559;

Best Local Similarity 45.6%;   Pred. No. 2.6e-66;
Matches 198; Conservative 51; Mismatches 113; Indels 72; Gaps 10;

Best Local Similarity 33.3%; Pred. No. 7.6e-56;
Matches 161; Conservative 97; Mismatches 184; Indels 42; Gaps 7;

```
Qy   58 GLPRRYIIAIMSGLGFCISFGIRCNLGVAIVSMVN----------NSTT-----HR 98
         |||  : ||||::||.| |:|||||||| |:|  : |||           |||||
Db   64 GPKTRHIFGFMGFLGFAVVYAMRVNLSVAIIVAMVNQTAIPHSNSSVIDTDTCPLPAPHHN 123

Qy   99 GGHVVVQK-AQFSWDPETVGLIHGSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTL 157
         |.:    :  ::.||| :||||.|||| |:|.||:|||::.::  :|:  : .:|.:|::|
Db  124 GSDPNPQKEGEFVWDEATQGLVAGSFFYGYVLTQVFPGGRMAELYGGKKIYGYGVLITAVF 183

Qy  158 NMLIPSAARVHYGCVIFVRILQGLVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAG 217
         :::.|:||. : ||.:|.||::|:.||||||| .|: |.| |||||.:.||  :.||:.|
Db  184 TLITPLAAHWDLPLLVLRILEGMGEGVTYPANHAMLAHWIPPLERNKFAAIVYAGSNIG 243

Qy  218 AVVAMPLAGVLVQ----YSGWSSVFYVYGSFGIFWYLFWLLVSYESPALHPSISEEERKYI 274
         :|::|||||:| .    ||.||:.||:.|  |:|::. |:||:|:.| .||.||:|.|.|:
Db  244 TVISMPLAGWLCSLDFLGGWPSAFYIFGLLGILMFIAWMYLVYDKPSDHPRISESEREYI 303

Qy  275 EDAI----------------------GSSAKLMNPLTKFSTPWRRFFSMPVYAIIVANFCRSWT 317
         |.:                       | .||:.::..|   .:|  |:.:|| |:|||:|||
Db  304 ERSLQVQRLINQDLAEAEEBEGQODEVSLRAPPSEPIPWSSLLTSVPLWAILLTQCGQGWA 363

Qy  318 FYLLLISQPDYFEEVFGFFEISKVGLVSALPHLVMTIIVPIGGQIADFLRSRRIMSTTNVR 377
         ||.  ::.|.||:.||| ||||||||||||||||||.|||||||||||||||||||||||
Db  364 FYTQLTELPTYMSNILHPDIQSNALLNAVPYLITSWFVGLTACSALADWMLARRYISILNSY 423

Qy  378 KLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVG-FSGFAISGFNVNHLDIAPRYASI 436
         ||:|  .  |||||||||||||||||||||| : |  |.|||.|||:|||||:||||:.|
Db  424 KLWNTVASVVPSLGLIGIIYVGCDWWVTFMLAGVGFGGAVYAGNQMNHIALSPRYAGT 483

Qy  437 LMGISNGVGTLLSGMVCPIIVGAMTKHK-TREEKWQYVFIIASLVHYGGVIFYGVFASGEKQ 495
         :|||:|  |||||||||||||||||||| |||:.||||:.||||||||||||||||||:||
Db  484 MYGITNSAANICGFLAPYVIGLLIINHRETLTQWHLVFWLAAGLNIAGNFIYLLFPASAEEQ 543

Qy  496 PWAE 499
         .| :
Db  544 SWSK 547
```

RESULT 6
US-11-097-143-27831
; Sequence 27831, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27831
; LENGTH: 516
; TYPE: PRT

; ORGANISM: DROSOPHILA
US-11-097-143-27831

Query Match 25.9%; Score 769.5; DB 7; Length 516;
Best Local Similarity 33.7%; Pred. No. 1.3e-53;
Matches 165; Conservative 97; Mismatches 192; Indels 35; Gaps 10;

```
Qy   43 TTQTRDPVVDCTCFGLPRRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRG---- 99
         |  |     |     ||| |::|:.::: |:|: | |||:|:||.:.|: |:|:||
Db   12 TEKDLEKPALGC----PATRYFVTFMLFLGMANAYVMRINMSVAIIVAMVNHTAIKSGEAE 67

Qy  100 -----GHVVV-----QKAQFSWDPETVGLIHGSFFWGYIVTQIPGGFICQKFAANRVFG 148
              |.|:.     :||.|.|  : .|:.||.|||||||:||:.||| |.:|:. : ||
Db   68 EYDDECGDRDIPIDDSQDGEFAWSSALQGYILSSFFYGYVLTQVFPGGILAKKYGSLRFLG 127

Qy  149 FAIVATSTLNMLIPSAAR---VHYGCVIFVRILQGLVEGVTYPACHGIWSKWAPPLERSR 205
         :.::.:||:.:|:|.||:   | :|.| :.|| |||.||||||| .|:.|||.||.||||
Db  128 YGMLINSVFAPLVPVAARGGGWVGLCA--VRFIQGLGEGPIVPCTHAMLAKWIPPNERSR 185

Qy  206 LATTAFCGSYAGAVVAMPLAGVLVQY---SGWSSVFYVYGSFGIFWYLFWLLVSYESPAL 262
         :.:.:..|:.:|:|::|||:|:| :    .||.|:||:.| ||:|:: | |:.:.:.|:|
Db  186 MGAAVYAGAQFGTIISMPLSGLLAEYGPDGGWPSIFYVPGIVGVTVWSIAPLIFVHEDPSS 245

Qy  263 HPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFSMPVYAIIVANFCRSWTFYLLL 322
         || | |:|.||::|::||.| |||.|    :  : ::|.| :|:|  :: :::.: :|
Db  246 HPTIDEREKKYINDSLWGTDVVKSP----PIPFKAIIKSLPFYAILFAIMGHNYGYETLM 301

Qy  323 ISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADFLRSRRIMSTTNVRKLMN- 381
         : .| ||.:: ::.|||.|::|:||:| :  :..|.  .|.::.| |:|:|..:::|:.
Db  302 TELPTYMKQVLRFSLKSNGLLSSLPYLAMWMLFSMEISVVADWMISSKRFSHTATRKLINS 361

Qy  382 CGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGFNVNHLDIAPRYASILMGIS 441
            .|||||||||||||||||||||||| :.||.||||.|||:|||||:||||:|:|||:
Db  362 IGQYGPGVALIAASYTGCDRALTLAILTIGVGLNGGGIYSGFKINHLDLTPRFAGFLMSIT 421

Qy  442 NGVGTLSGMVCPIIVGAMTKHKTRE---EWQYVFLIASLVHYGGVIFYGVFASGEKQPWA 498
         |  ::|:|::.|:::|.   ::.|:   .||:||.||: :.|:|:|||.:|.|||:||: .
Db  422 NCSANLAGLLAPIAAGHLISDPSSKPMMGQWQIVFPIAAFVYIIGGTFYNIFGSGERQYND 481

Qy  499 EPEEMSEEK 507
         ||: : ||:
Db  482 NPED-DEQK 489
```

RESULT 7
US-11-097-143-17844
; Sequence 17844, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17844
; LENGTH: 529
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-17844

Query Match   25.8%; Score 767.5; DB 7; Length 529;
Best Local Similarity   34.5%; Pred. No. 2e-53;
Matches 164; Conservative 94; Mismatches 185; Indels 33; Gaps 10;

```
Qy   56  CFGLPRRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRG------:------GHVVV--  104
             :|::|:|:||:|::|:|: |::||| |||||||:|:            |||
Db   36  CPA--TRYFVTFMFLGMANAYVMRINMSVAIVAMVNHTAIKSGEABEYDDECGDRDIPI  93

Qy  105  ---QKAQFSWDPETVGLIHGSFFWGYIIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLI  161
            ::|:|:|||||||:||||||||||||||||:|||:::|:|:|:||:|||::  :
Db   94  DDSQDGEFAWSSALQGYILSSFFYGYIVTQIPFGILAKKYGSLRFLGYGMILNSVFAFLV  153

Qy  162  PSAAR---VHYGCVIFVRILQGLVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGA  218
             |||    |||||||||||||||||||||||||||||||||||||||||||||:
Db  154  PVAARGGGVWGLCA--VRFIQGLGEGPIVCTHAMLAKWIPPNERSRMGAAVYAGAQFGT  211

Qy  219  VVAMPLAGVLVQY---SGWSSVFYVYGSFGIFWYLFWLLVSYESPALHPSISEEERKYIE  275
             :::|||||||: |      :|| |||:|:||||:||||||:::||:|:|:|:||||
Db  212  IISMPLSGLLAEYGPDGGWPSIFYVFGIVGTVWSIAFLIFVHEDPSSHPTIDEREKKYIN  271

Qy  276  DAIGESAKLMNPLTKFSTPWRRFFTSMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGF  335
             |:::|:||:|||||:|||::|: |:||||:||||||||||||||:|||||||:||:||||
Db  272  DSLWGTDVVKSP----PIPFKAIIKSLPFYAILFAIMGHNYGYETLMTELPYTMYKQVLRF  327

Qy  336  EISKVGLVSALPHLVMTIIVPIGGQIADFLRSRRIMSTTNVRKLMN-CGGFGMEATLLLV  394
             |:||||||||||||||||||||||||||||||||||||||||||| |||||||||||:
Db  328  SLKSNGLLSSLPYLAMWLFSMFISVVADWMISSKRFSHTATRKLINSIGQYGPGVALIAA  387

Qy  395  VGYSHSKGVAISFLVLAVGFSGFAISGGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPI  454
             |||:|::|||||||||||::||:||:||||:|||:||||||||||:|||||||:|:|||
Db  388  SYTGCDRALTLAILIIGVGLNGGIYSGFKINHLDLTPRFAGPLMSTTNCSANLAGLIAPI  447

Qy  455  IVGAMTKHKTRE------EWQYFLIASLVHYGCVIFYGVFAASGEKQPWAEPEEMSEEK  507
             :|||:|||:||       |||||||||||||||||||||||||||||||:|:|||::|
Db  448  AAGHLISDPSKPMMGQWQIVFFIAAFVYIICGTFYNIFGSSGERQYWDNPED-DEQK  502
```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5532
; LENGTH: 493
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-5532

Query Match   25.2%; Score 747; DB 7; Length 493;
Best Local Similarity   33.3%; Pred. No. 8.1e-52;
Matches 158; Conservative 93; Mismatches 187; Indels 36; Gaps   8;

```
Qy   58  GLPR--------RYIIAIMSGLGFCISFGIRCNLGVAIVSMVN----------------  92
             |||         ||:|:|:||:|:|:|||||||||||||:|
Db    8  GLQRVRNFLSCRQVINLLITMLGFMLNYALRVNLTIAIVDMVRPNVTSAVNATLVGNSTAA  67

Qy   93  NSTTHRGGHVVVQKAQFSWDPETVGLIHGSFFWGYIIVTQIPGGFICQKFAANRVFGFAIV  152
             ||:        :::||||||||||||||||||||||||||||||:|:|:||||||||
Db   68  NSTASPDG--VDVYEERFPWDSYQTNFVLGCFFWGYILTELPGGRLAELIGGRVVFGHSML  126

Qy  153  ATSTLNMLIPSAARVHYGCVIFVRILQGLVEGVTYPACHGIWSKWAPPLERSRLATTAFC  212
             |||:|||||||:||||||||||||||||||||||||||||||||||||||||||||:|
Db  127  WASLLTLITPLARAHINVVLLIVVRVLGFMLGASWPAIHPVAAVWIPPMERSKFMSNNMA  186

Qy  213  GSYAGAVVAMPLAGVLVQYSGWSSVFYVYGSFGIFWYLFWLLVSYESPALHPSISEEERK  272
             |||||| :|||||||:|:||||||||:|||:|||||:||||||:|:|||:|||:|:||
Db  187  SS-LGAAITMPICGYLISVAGWASVFYLTGAVGLLWSLAWFFVYEIPATHPRISAEERR  245

Qy  273  YIEDAIGESAKLMNPLTKFSTPWRRFFTSMPVYAIIVANFCRSWTFYLLLISQPDYFEEV  332
             ||||:||||||||||||:|||::|::|:||||:||||||||||||||||||||||||:
Db  246  EIEEAIGTTTSKKRP----SHVPWGQLLCSPAVWAIIICHLGLAVFGFTIVVNQLPTFMSKI  302

Qy  333  FGFEISKVGLVSALPHLVMTIIVPIGGQIADFLRSRRIMSTTNVRKLMNCGGFGMEATLL  392
             |||||||||||||||||||||||||||||||||||||||||||||:|:||:||||||||:
Db  303  LHFDIKQNGLFSSLPYLGKYVNVAVASSYLADYLRKKGTLSTTATRKLFTTFALVIPGLLM  362

Qy  393  LV----VGYSHSKGVAISFLVLAVGFSGFAISGGFNVNHLDIAPRYASILMGISNGVGTLSG  449
             |      |||:|::|||||||||||::||:||:||||:|||:|||||||||:|||||||:
Db  363  IVQVFLGYDATWSVTI--FSLALFAHGAVTAGYLGNGLDIAPNFGGTIFGLANTLSSFGG  420

Qy  450  MVCPIIVGAMT-KHKTRBEEWQYVFLIASLVHYGCVIFYGVFAASGEKQPWAEPEE  502
             |:|||:|||:| |:|::||||:|||||||||||||||||||||||||||||:|:|
Db  421  FLSTSMVGALTYKDQSFHSWQIVFWILAATYISAAVVFAILGSGELQPWNNPPE  474
```

RESULT 8
US-11-097-143-5532
; Sequence 5532, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
;   et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008

RESULT 9
US-60-669-241-29729
; Sequence 29729, Application US/60669241
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Baum, James A
; APPLICANT: Gilbertson, Larry A
; APPLICANT: Kovalic, David K
; APPLICANT: LaRosa, Thomas J
; APPLICANT: Lu, Maolong
; APPLICANT: Munyikwa, Tichifa R. I.
; APPLICANT: Roberts, James K
; APPLICANT: Wu, Wei
; APPLICANT: Zhang, Bei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CONTROL OF INSECT INFESTATION IN PLA
; FILE REFERENCE: 38-21(53596)
; CURRENT APPLICATION NUMBER: US/60/669,241
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60560842
; PRIOR FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60565632
; PRIOR FILING DATE: 2004-04-27
; PRIOR APPLICATION NUMBER: 60579062
; PRIOR FILING DATE: 2004-06-11
; PRIOR APPLICATION NUMBER: 60603421
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: 60617261
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 50011

```
; SEQ ID NO 29729
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Lygus hesperus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (436)..(436)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; OTHER INFORMATION: Coding regions on vcDNA
; FEATURE:
; OTHER INFORMATION: Homolog annotation: Hit_ID=XP_317786.1; Match level="QueryCoverag
; OTHER INFORMATION: =89%, HitCoverage=92%, E-value=1e-134, Identity=50%"; Hit descrip
; OTHER INFORMATION: ENSANGP00000022197 [Anopheles gambiae]
; FEATURE:
; OTHER INFORMATION: Gene Ontology Annotation: Molecular function=inorganic phosphate
; OTHER INFORMATION: transporter activity; Cellular component=integral to membrane;
; OTHER INFORMATION: Biological process=phosphate transport
; FEATURE:
; OTHER INFORMATION: Pfam annotation: Pfam_ID=MFS_1; Match level="Score=203.1, E-value
; OTHER INFORMATION: =5.6e-58, Copies=1"; Pfam description=Major Facilitator Superfami
US-60-669-241-29729

Query Match      24.4%;   Score 726;  DB 8;  Length 477;
Best Local Similarity   33.0%;  Pred. No. 3.8e-50;
Matches 141; Conservative 88; Mismatches 178; Indels 20; Gaps 3;

Qy   59  LPRRYIIAIMSGLGFCISFGIRCNLGVAIVSMNNSTTHRGGHVVVQKA--            107
             :||||:|:||:|||:|| |:|||||||||:| |  |   |  |
Db   26  IPQRYVLGLMGFLAVANAYAMRGILNLAITEMVVNPKNKAHHVVDDNACPGILEVKNHT    85

Qy  108  ---QFSMDPETVGLIHGSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPS   163
             |||||:|||:|||||||||||||||||||||||||||||||||:||:
Db   86  DPNNEFDWDEQTQGYILSAFYWGYVLTLHLPGGLLAQRGGKQTLGLGTLGTAVLTLTPF   145

Qy  164  AARVHYGCVIFVRILQGLVEGVTYPACHGIWSKWAPPLERSRLAATTAFCGSYAGAVAMP   223
         |||  |  |||:|||:|||:|||||||||  ||:  ||||||:|
Db  146  AARAGPNWLIAVRLLEGLGEGTTFPPALNQLLAQWVPPLERGRLGSLVPAGNQIGTVVSSA  205

Qy  224  LAGVLVQYSGWSSVFYVVGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAK   283
         |:|:| | ::||::||:|:|:|:|| :||:||||:|||:|::| |:  |:|::||  |
Db  206  LSGLLLDVYDWPIILYIFGSAGVLWVFWIFLCYNDPASHPFITEKEKDYLEETIGGIKR    265

Qy  284  LMPLTKFSTPWRRFFTSMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLV    343
              | |||:||  | |  |  ||| :   || ||||||||:|| |: |
Db  266  KEH----LRVPWGSMATSLPLWALIIIGQIGHDWGLFIQTDLPKYMKSVSVMKFSIVQNGIL   321

Qy  344  SALPHLVMTIIVPIGGQIADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGV   403
         ::||:|||  ||| ||:||||| |||:|||||:||||:  ||  |:||:|
Db  322  TSLPFLVMWFTAIGAGILGDFLLKCKVWSVTVCRKVFTTIASVGPALCGVILASYAGCDRV  381

Qy  404  AISFL-VLAVGFSGFAISGFRNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKH  462
         |::   ||| |||||| |||:|:|||||:||||||||:|:|:|| ||::|||:|||
Db  382  AAATLFTVGMAFMGFFYPSLKVNALDLSPNYAGTIMALVNGIGAISGIITPTLIXYLTPD   441

Qy  463  KTREEWQ    469
          |  ||
Db  442  QTMMEWR    448
```

```
; PRIOR APPLICATION FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR APPLICATION FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR APPLICATION FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR APPLICATION FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR APPLICATION FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR APPLICATION FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR APPLICATION FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR APPLICATION FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SEQ ID NO 11013
; TYPE: PRT
; ORGANISM: DROSOPHILA
; LENGTH: 496
; SOFTWARE: FastSEQ for Windows Version 4.0
US-11-097-143-11013

Query Match      24.2%;   Score 719.5;  DB 7;  Length 496;
Best Local Similarity   32.6%;  Pred. No. 1.3e-49;
Matches 163; Conservative 92; Mismatches 192; Indels 53; Gaps 12;

Qy   57  FGLPRRYIIAIMSGLGFCISFGIRCNLGVAIVSMV--NNST---------THR         98
          |:|:|||:|||||:|| |:|||||||||||||:     |:         |
Db   15  FVIPQRVILAIMGFLAILNAYTMRVCLSQOAITVLVVKKNSTDDDSEAICEPDDIDEGTSV   74

Qy   99  GGHVVVQKAQFSWDPETVGLIHGSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLN   158
         ||    | :|:  |:| |||:|||| :||||| :|||||||||:
Db   75  GG----DFEWSEELQGSLILSSFYIGIVTHIPGGLLAEKFGGKWTLGLGLISTAVFT    127

Qy  159  MLIPSAARVHYG---CVIFVRILQGLVEGVTYPACHGIWSKWAPPLERSRLAATTAFCGSY   215
         ||:| ||  |     |||:|||:|||:|||||||| |  ||||:|||||||:|
Db  128  MLTPLA--INKGDSDWLIVTRVLMGLGEGTTFPPALSVLLAAWVPANERGKLGALVLGGGQ   185

Qy  216  AGAVVAMPLAGVLVQYSGWSSVFYVVGSFGIFWYLFWLLVSYESPALHPSISEEERKYIE   275
                 |:|:|||| ::||::||:|:|:|:|||:||:||||:|||:|::|  |:|:|
Db  186  VGTIMGNLLSGGVFIIDAYGWEFVFYFGGGLGVVWFAIFWFLCYSDPTSHPFIKPSEREYLV  245

Qy  276  DAIGESAKL--MNPLTKFSTPWRRFFTSMPVYAIIVANFCRSWTFYLLLISQPDYFEEVF   333
          ||| |     || |||:||  | |  | ||| :| || | ||||||||:||
Db  246  KEIGTISRNEDLPP------TPWKAILTNLPMPALVAAQIGHDWGFYIMVTDLPKYMADVL   300

Qy  334  GFEISKVGLVSALPHLVMTIIVPIGGQIADFLRSRRIMSTTNVRKLMNCGGFGMEATLLL   393
         ||:||:  | ::||:|||  ||| ||:||||| |||:|||||:||||:
Db  301  QFSIKANGLYXSSLPYVMMWIVSVSSGFVADWMIRRGVLSTTNTRKVMT--GLAAPGPAIF  358

Qy  394  VVGYSHS---KGVAISFLVLAVGFSGFAISGFRNVNHLDIAPRYASILMGISNGVGTLSGM   450
         |:|||:    |  |::  ||| |||||| |||:|:|||||:||||||||:|:|:||
Db  359  MVGASYAGCDRVLVVVLFTICMGLMGAYYAGMKLSPLDMSPNYAGTIMAITNGIGAITGV   418

Qy  451  VCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVIFYGVFASGEKQPW-----AEPE----E  502
         |||:||| |||| |  ||::||:|||:|::||||:||||||: |||     | |    |
Db  419  ITPYLVGVNMTPNASLLEWRLVFWWAFGVLCFTAVIYCIWASGEVQPFNNAPIQPRSVDFE   478

Qy  503  MSEEKCGFVGHDQLAGSDDS   522
          :|:| |:  ::  |:
Db  479  AQERK---VGGEKTSGLEQS   495
```

; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20922
; LENGTH: 465
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-20922

Query Match   24.1%; Score 716.5; DB 7; Length 465;
Best Local Similarity   31.8%; Pred. No. 2.1e-49;
Matches 143; Conservative 107; Mismatches 189; Indels 11; Gaps 6;

Qy   56 CFGLPRRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVV-----QKAQFSW 111
              |||||||||| | | |:| :||
Db   6 CFYVPKRINLAIMLFMACLLSYMMRVNLSINIIAMVEDTSSHENGTEVEALPDYGPRYNW 65

Qy   112 DPETVGLIHGSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGC 171
              |:||||||| |||||||||:|||||||||||||||||||||||:|||| ||:||
Db   66 TQSDQALILGAYFYGYMITSLPAGTLAEMLGARNVAGYSCLIVAGILTALTPAAAAWDKYA 125

Qy   172 VIFVRILQGLVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQY 231
              |:||| | || ||||:| || || | | |:|| |||| | || | |: :|
Db   126 VFAVRFLIGFLNGVVYPCCHSLVSKWSPPDEKGKFVASLMGGTF-GTVITWPISGVIEN 184

Qy   232 SGWSSVFYVYGSFGIFWYLFWLLVSTESPALLHPSISEEERKYIEDAIGESAKLMNPLTKF 291
              ||||||:||:||||:|||||||||| :| ||||: | |:| |::|:||||||
Db   185 LGWDWAPYIVGIFVVLVVVAIWFYLVADTPAQHSTISLKEREYIESSLGDT--LSN--KKK 240

Qy   292 STPWRRFFTSMPVYAIIVANFCRSWTFYLLLISQPDYFEEVEGFEISKVGLVSALPHLVM 351
              |:| | | :|| |||| | |||: || |||| | |:||||| ||||
Db   241 WPPYKELVLSLPFWSLMMLHYGSMWGLFFLITATPKFLSEVLGFNLSSAGFLSSLPHVAR 300

Qy   352 TIIVPIGGQIADFLRSRRIMSTTNVRKLMNCGGFGMEATLLIVVGY-SHSKGVAISFLVL 410
              |||: | || | | |: | | |: | | | :|| : | | |: |
Db   301 LLCAFGFGAVADWIRRRGWLSVTRMRKAFCLPSHILPGVMLIILAYFGRDPYVCVAIMTI 360

Qy   411 AVGFSGFAISGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHK-TREEWQ 469
              | |:|| | | |:| ||:|||:| | | |||:| |:| |: ::|| :||||
Db   361 SLGFNGAATASNLANSQDLIAENYAGTLYGINCVGTTPGIFSPLIVAAFTKNENTIDQWH 420

Qy   470 YVFLIASLVHYGGVIFYGVFASGEKQPWAE 499
              | |: ||:|: |:|: |||| :| ||
Db   421 WVFIIGAAAYILPALFPWVFGSGKIQKWNE 450

; APPLICANT: Lu, Maolong
; APPLICANT: Munyikwa, Tichifa R. I.
; APPLICANT: Roberts, James K
; APPLICANT: Wu, Wei
; APPLICANT: Zhang, Bei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CONTROL OF INSECT INFESTATION IN PLA
; FILE REFERENCE: 38-21(53597)
; CURRENT APPLICATION NUMBER: US/60/669,175
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60560842
; PRIOR FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: 60556632
; PRIOR FILING DATE: 2004-04-27
; PRIOR APPLICATION NUMBER: 60579062
; PRIOR FILING DATE: 2004-06-11
; PRIOR APPLICATION NUMBER: 60603421
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: 60617261
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 40774
; SEQ ID NO 21828
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Diabrotica virgifera
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (147)..(148)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (166)..(166)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (172)..(172)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (181)..(181)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; OTHER INFORMATION: Coding regions on vcDNA: vcDNA=SeqID_1525; Strand=+; Position=189
; FEATURE:
; OTHER INFORMATION: Homolog annotation: Hit ID=EAL31894.1; Match level="QueryCoverage
; OTHER INFORMATION: =92%; HitCoverage=89%, E-value=1e-160, Identity=63%"; Hit descrip
; OTHER INFORMATION: GA18114-PA [Drosophila pseudoobscura]
; FEATURE:
; OTHER INFORMATION: Gene Ontology Annotation: Molecular function=inorganic phosphate
; OTHER INFORMATION: transporter activity; Cellular component=integral to membrane;
; OTHER INFORMATION: Biological process=phosphate transport
; FEATURE:
; OTHER INFORMATION: Pfam annotation: Pfam ID=MFS_1; Match level="Score=180.8, E-valu
; OTHER INFORMATION: =2.9e-51, Copies=1"; Pfam description=Major Facilitator Superfami
US-60-669-175-21828

Query Match   23.8%; Score 708; DB 8; Length 465;
Best Local Similarity   33.4%; Pred. No. 1e-48;
Matches 155; Conservative 91; Mismatches 176; Indels 42; Gaps 11;

Qy   24 LGVAIVSMVN----------------------NSTTHRGGHVVVQKAQFSWDPETVGLIHGSFF 124
              | |||:|:| || | | || || |:|| |||||||||
Db   9 ESNGEESDTESVYED-EDETTRILPPEVEDTTNC--CFGLPRRYIIAIMSGLGFCISFGIRCN 66

Qy   66 LSVAIVAMVNTTQPVFFTNNSYDHCIPITDNSTNTNG---TATPGEFDWDEKTQSIVLGSFF 122
              ||| | | | :| :|| :| :| | |: |: ||:| ||| ||||
Db   67 WGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQGL-VE 183

Qy   125 YGVVLTQVPGGRLAEIFGSKRVYGXXVLVTSIFTLLTPIAARMXIHYLLXVRVLEGMGXE 182
              | | :|| || | | |||:: |:|| |: ||| ||| :|||| :|||| | |
Db   123 GVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQY---SGWSSVFYV 184

Qy   184 GVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQY---SGWSSVFYV 240
              |||: | | | | |||:
Db ||| :

RESULT 12
US-60-669-175-21828
; Sequence 21828, Application US/6069175
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Baum, James A
; APPLICANT: Gilbertson, Larry A
; APPLICANT: Kovalic, David K
; APPLICANT: LaRosa, Thomas J

RESULT 13

```
Db  183  GVTFPSMYAMLARWIPPLERSKFAAYVYAGTNFGTILSLPISGWLCSLKLDNGWPLSFYI  242
              :|||:|   |      |||  ||      :  |||    :|  |||       |
Qy  241  YGSSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT  300

Db  243  FGVLGIVWLFWLLIYDTPMSHPRIDPQEKAFILASIGP----QDDRDTSSIPWKHMLR    298
         |  || |||||||  |        :|: |         |         ::  | |
Qy  301  SMPVYAIIVANFCRSWTFYLLLISQPDYFPEEVFGFEISKVGLIVSALPHLVMTIIVPIGGQ  360

Db  299  CMPLWAILLVTQCGQSWAFYTQLITELPTYMAQILHFDIQSDALLSAVYFTSW----IGGI   354
              | | |: ||:  |  |      |         |::    |: |:|
Qy  361  I-----ADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVUGYSHSKGVAISFLV-LAVGFS   415

Db  355  LFSIFADWLLSKGYLSLSTSYKVFNSVASVIPSIGLLGVAYVGCDKVAAQLLLALTATFG   414
         || |   ::   | |:     :|    |  | |  |||  |      |: |    | |
Qy  416  GFAISGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAM                  459

Db  415  GAVYAGNQMNHIALSPQYAGTMYGITNSAAMMCCFLAPYVIGLL                  458
```

```
; GENERAL INFORMATION:
;   APPLICANT: Venter, J. Craig
;   et al.
;   TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;   TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;   TITLE OF INVENTION: DROSOPHILA GENES.
;   FILE REFERENCE: CL000728
;   CURRENT APPLICATION NUMBER: US/11,097,143
;   CURRENT FILING DATE: 2005-04-04
;   PRIOR APPLICATION NUMBER: 60/157,832
;   PRIOR FILING DATE: 1999-10-05
;   PRIOR APPLICATION NUMBER: 60/160,191
;   PRIOR FILING DATE: 1999-10-19
;   PRIOR APPLICATION NUMBER: 60/161,932
;   PRIOR FILING DATE: 1999-10-28
;   PRIOR APPLICATION NUMBER: 60/164,769
;   PRIOR FILING DATE: 1999-11-12
;   PRIOR APPLICATION NUMBER: 60/173,383
;   PRIOR FILING DATE: 1999-12-28
;   PRIOR APPLICATION NUMBER: 60/175,693
;   PRIOR FILING DATE: 2000-01-12
;   PRIOR APPLICATION NUMBER: 60/184,831
;   PRIOR FILING DATE: 2000-02-24
;   PRIOR APPLICATION NUMBER: 60/191,637
;   PRIOR FILING DATE: 2000-03-23
;   NUMBER OF SEQ ID NOS: 43008
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28257
;   LENGTH: 475
;   TYPE: PRT
;   ORGANISM: DROSOPHILA
US-11-097-143-28257
Sequence 28257, Application US/11097143
```

```
Query Match      23.6%;   Score 699.5;  DB 7;  Length 475;
Best Local Similarity   33.1%;   Pred. No. 5.1e-48;
Matches  149;  Conservative  91;  Mismatches 197;  Indels  13;  Gaps  6;
```

```
Qy   58  GLPRRYIIAIMSGLGFCISFGIRCNLGYAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVG  117
         || ||| :::::|:|| |: |||||||| : ::: :         || |:
Db   16  GLGVRHFQVLLFFALTVAYGCRVNLSVAVVAMTDAAS-----VNPDFPEYNWSEKTKS    69

Qy  118  LIHGSFFWGYVITQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARV-HYGCVIFVR  176
         || ||||||| | :|:|| | :|:||| || :: ||| |:|| || ||    :|| :: |
Db   70  LILSSFFWGYVITQVPAGQLARKYGGKVMILSGLAICSILNILTPICAKIGGWQLVCALR  129

Qy  177  ILQGLVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYS-GWS  235
         :::||::|| :|: |:||  ||||:::  |  :: |  | |  :::|:|::| :   ||
Db  130  VVEGLCQGVVFPSTHTILSQWAPPEKERATLGTCAYSGNQPFGTIIMLATSGVIAASPIGWP  189

Qy  236  SVFYVYGSFGIFWYLFWLLVSYESPALHPSISEEERKYIE--DAIGESAKLMNPLTKFST  293
          :   |
Db  236  |                                                           293
```

RESULT 14

```
Db  190  SIFYISGGIGCWSVVYFFGAGSPQECKSISAEEKKLIEMSQADEVSGGQEHQPKEQLPT  249
                 :    ||       |           :    :     |  |: | |
Qy  294  PWRRFFTSMPVYAIIVANFCRSWTFYLLLISQPDYFPEEVFGFEISKVGLIVSALPHLVMTI  353

Db  250  PWLSFFTSPAFLVILVSHSVHNWGFWTLLTEIPSYMKNIIGKDIKSNALLSSLPVVCMFA  309
                   |  || :|        |   :                 :
Qy  354  IVPIGGQIADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLIVVGYSH--SKGVAISFLVLA  411

Db  310  MSFVFSSISAQLNRNRNCISRSTSRKLFNSIGLIWIPMVTLVGIGYVNPDQSELAVVLLCFT  369
                 :                          |:  ||
Qy  412  VGFGCFAISGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVG-AMTKHKTREEWQY  470

Db  370  VGMNGATTLGFNTNHIDLSPNFAGILMGITNGVANIMSTIAPLLVGFIVTNEHDPEQWRI  429
                    |                 |:         |
Qy  471  VFLIASLVHVGGVIFYGVFASGEKQPWAEP                              500

Db  430  VFFIAAGFYLVGNTLYVIFGKANVQPWNDP                              459
```

```
; GENERAL INFORMATION:
;   APPLICANT: Venter, J. Craig
;   et al.
;   TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;   TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;   TITLE OF INVENTION: DROSOPHILA GENES.
;   FILE REFERENCE: CL000728
;   CURRENT APPLICATION NUMBER: US/11,097,143
;   CURRENT FILING DATE: 2005-04-04
;   PRIOR APPLICATION NUMBER: 60/157,832
;   PRIOR FILING DATE: 1999-10-05
;   PRIOR APPLICATION NUMBER: 60/160,191
;   PRIOR FILING DATE: 1999-10-19
;   PRIOR APPLICATION NUMBER: 60/161,932
;   PRIOR FILING DATE: 1999-10-28
;   PRIOR APPLICATION NUMBER: 60/164,769
;   PRIOR FILING DATE: 1999-11-12
;   PRIOR APPLICATION NUMBER: 60/173,383
;   PRIOR FILING DATE: 1999-12-28
;   PRIOR APPLICATION NUMBER: 60/175,693
;   PRIOR FILING DATE: 2000-01-12
;   PRIOR APPLICATION NUMBER: 60/184,831
;   PRIOR FILING DATE: 2000-02-24
;   PRIOR APPLICATION NUMBER: 60/191,637
;   PRIOR FILING DATE: 2000-03-23
;   NUMBER OF SEQ ID NOS: 43008
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37224
;   LENGTH: 491
;   TYPE: PRT
;   ORGANISM: DROSOPHILA
US-11-097-143-37224
Sequence 37224, Application US/11097143
```

```
Query Match      23.6%;   Score 699.5;  DB 7;  Length 491;
Best Local Similarity   33.1%;   Pred. No. 5.3e-48;
Matches  149;  Conservative  91;  Mismatches 197;  Indels  13;  Gaps  6;
```

```
Qy   58  GLPRRYIIAIMSGLGFCISFGIRCNLGYAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVG  117
         || ||| :::::|:|| |: |||||||| : ::: :         || |:
Db   32  GLGVRHFQVLLFFALTVAYGCRVNLSVAVVAMTDAAS-----VNPDFPEYNWSEKTKS    85

Qy  118  LIHGSFFWGYVITQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARV-HYGCVIFVR  176
         || ||||||| | :|:|| | :|:||| || :: ||| |:|| || ||    :|| :: |
Db   86  LILSSFFWGYVITQVPAGQLARKYGGKVMILSGLAICSILNILTPICAKIGGWQLVCALR  145

Qy  177  ILQGLVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYS-GWS  235
         :::||::|| :|: |:||  ||||:::  |  :: |  | |  :::|:|::| :   ||
Db  146  VVEGLCQGVVFPSTHTILSQWAPPEKERATLGTCAYSGNQPFGTIIMLATSGVIAASPIGWP  205

Qy  236  SVFYVYGSFGIFWYLFWLLVSYESPALHPSISEEERKYIE--DAIGESAKLMNPLTKFST  293
          :   |
Db  236  |                                                           293
```

```
Db   206 SIPYISGGIGCVWSVVYFFPGAGSPQOECKSISAEEKKLIEMSQADEVSGGGQEOPKEQLPT 265
             :| |          |    | |      | |  ||     |    |
Qy   294 PWRRFFTSMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTI 353
         :|:||   |  ||   | :||  ||| :|  : |:|| |  ||||
Db   266 PWLSFFTSPAFLVLIVSHSVHNWGFWTLLTEIPSYMKNILGKDIKSNALLSSLPYVCMFA 325

Qy   354 IVPIGQOIADFLRSRRIMSTNVRKLMNCGFGMEATLLLVVGYSH--SKGVAISFLVIA 411
         |||| :|||||||||||||||: ||||                  |:|:||:|||:
Db   326 MSFVFSSISAQLNNRINCISRSTSRKLPFNSIGLWIPMWTLVGLGYVNPDQSELAVVLLCFT 385

Qy   412 VGFSGFAISGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVG-AMIKHKTREEWQY 470
         || |||||||||||:||||||||:|||| |||||||||||||||  |: |:|||||| |
Db   386 VGMNGATYLGFNTNHIDLSPNFAGILMGITNGVANIMSIIAPLIVGPIVTNEHDPEQWRI 445

Qy   471 VFLIASLVHYGGVIFYGVFASGEKQPWAEP 500
         || | |  |:||  |: |||:||| ||::|
Db   446 VFFIAAGFYLVGNTLYVIFGKANVQPWNDP 475
```

```
Db   196 VMSTIIYVGTSAGTALSILLAGVCSAQWGWESVFYVMGALSCIWMLLWVILVQDNPNKQR 255
            |:  ||||  |  |||:| |||  |      |||: |||    | : :| :|||| :|
Qy   265 SISEEERKYIEDAIGESAKL-MNPLTKFSTPWRRFFTSMPVYAIIVANFCRSWTFYLLLI 323
          |:||  | |    |  |:|     | |: ||: | |  |     |:||   || :|
Db   256 FISLEERQMITSSLGTEQKTEHHP---AVPWGKVFTSVPFWAILIAHTCSNFGWYMFLI 311

Qy   324 SQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQOIADFLRSRRIMSTTNVRKLMN-- 381
           ||:||| |  ||||||||||||||||||| | |  :|||||||||||||||: ||||
Db   312 EIPFYMKQVLKFNVASNAALSALPYFPMIIFSICLGKLLDDSLQAKGKITTTVARKTATSI 371

Qy   382 CGGF-GMEATLLLVVGYSHSKGVAISFLVLAVGF--SGFAISGFNVNHLDIAPRYASIIM 438
            |  || |:|||| ||| : | ||:|||:| |    ||||||||||||:||||||||:|
Db   372 CTLIPGVCLLVLCYIGCRHYEAVS----VMSVGIVAMGSMFGGFLSNHIDIAPNFAGTLV 427

Qy   439 GISNGVGTLSGMVCPIIVGAMTK-HKTREEWQYVFLIASLVHYGGVIFYGVFASGEKQPW 497
         || ||||||||||||||||:| | |:|||||| || | |  |:||  |: |||:||| ||
Db   428 ALTNTAATLPGIVUPLFVGFVTIKGNQNIGAWRIIFGVTIVLFALEFLVVFLGSGSGSEQPW 487

Qy   498 AEPEEMSEEKCGFVGHDQLAGS-DDSEMEDEAEPPGAPPAPP 538
          |:: |                  | :|
Db   488 NK-------------AGTPKDPEAKDEKTPLKELPTKP 512
```

RESULT 15
US-11-097-143-9567
; Sequence 9567, Application US/1097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SEQ ID NO 9567
; LENGTH: 512
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-9567

```
Query Match      23.5%;  Score 698.5;  DB 7;   Length 512;
Best Local Similarity   30.7%;  Pred. No. 6.7e-48;
Matches  160;  Conservative 103;  Mismatches 192;  Indels 67;  Gaps 12;

Qy    59 LPRRYIIAIMSGLGFCISFGTRCNLGVAIVSMVNNST--TH-----RGGH---------- 101
         :||:|||  |:  |  |  | |:| | ||||||:
Db    16 VPARVLALLGSIGMAIVYGLKVNLSVAMVAMVNHTAIKAHGDGGHGHGSVILSNASQ 75

Qy   102 ----------VVVOKAQPSWDPETVGLIHGSFFWGYIVTVQIPGGFICQKFAAN 144
                    |::||: | | | ||  ||| |:||||||:  |||| | | ||
Db    76 VSLVEECNPPGGASNTAKVEDGPFDWSEPLOGTLLSCYFWGYLVSQOIPLAHVAENFSAK 135

Qy   145 RVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEGVTVYPACHGIWSKWAPPLERS 204
          | | |||:|:| |:| |: |: |||:| | |:|| | || || |  :|:|| || |: |
Db   136 WVMLFSVAINVVCTLLTPVFTELHYGGLILMRVLEGVGGGASFPAMHVMIASWAPPTERM 195

Qy   205 RLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYYGSFGIFWYLFWLLVSYESPALHP 264
         :|::||  ||:|| ||| | |  ||  || :| | :  | :|| |||:|::|:||||
```

Search completed: June 2, 2005, 11:42:03
Job time : 58 secs

OM protein - protein search, using sw model

Copyright (c) 1993 - 2005 Compugen Ltd.

GenCore version 5.1.6

Run on: June 2, 2005, 11:20:37 ; Search time 42 Seconds
                                         (without alignments)
                                         1282.890 Million cell updates/sec

Title: US-10-734-731-4
Perfect score: 2970
Sequence: 1 MEFRQEEFRKLAGRALGKLH............YGATHSTFQPPRPPPVRDY 560

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   1:   PIR_79:*
                 1:   pir1:*
                 2:   pir2:*
                 3:   pir3:*
                 4:   pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2925	98.5	560	2	I59302	brain specific Na+
2	1297	43.7	576	2	H88548	protein ZK512.6 [1
3	1294	43.6	563	2	T43650	probable sodium-de
4	971	32.7	573	2	T23589	hypothetical prote
5	950	32.0	544	2	T24633	hypothetical prote
6	885	29.8	466	2	S40767	hypothetical prote
7	775.5	26.1	493	2	G88553	protein C3BC10.2 [
8	763.5	25.7	472	2	S28286	hypothetical prote
9	720.5	24.3	512	2	H84698	hypothetical prote
10	685.5	23.1	465	2	A56410	sodium/phosphate t
11	626.5	21.1	467	2	A48916	sodium phosphate t
12	619	20.8	465	2	S69915	sodium-phosphate t
13	616.5	20.8	465	2	I39473	Na+-dependent phos
14	596.5	20.1	413	2	T01534	hypothetical prote
15	471	15.9	537	2	T45634	hypothetical prote
16	466.5	15.7	561	2	D84800	hypothetical prote
17	455.5	15.3	501	2	B89135	protein F25G6.7 [i
18	439.5	14.8	380	2	S44742	hypothetical prote
19	423.5	14.3	568	2	T25419	C02C2.4 protein -
20	422	14.2	592	2	T24729	hypothetical prote
21	403	13.6	516	2	T23590	hypothetical prote
22	396	13.3	445	2	T29418	hypothetical prote
23	394	13.3	530	2	AE0861	hypothetical prote
24	387.5	13.3	452	2	A65061	probable glucarate
25	385.5	13.0	450	2	C85930	probable glucarate
26	385.5	13.0	450	2	A91085	probable transport
27	385.5	12.5	450	2	T29968	probable transport
28	373	12.6	506	2	T15201	hypothetical prote
29	371.5	12.5	499	2		hypothetical prote
30	363.5	12.2	425	2	A90055	hypothetical prote
31	361	12.2	485	2	T24115	hypothetical prote
32	356	12.0	455	1	H69752	probalble glucarat
33	338	11.4	659	2	T33557	hypothetical prote
34	337	11.3	543	2	T32496	hypothetical prote
35	330.5	11.1	444	2	E85974	probable galactara
36	330.5	11.1	444	2	E91129	probable galactara
37	330.5	11.1	444	2	C65102	probable galactara
38	329.5	11.1	487	2	S44900	probable galactara
39	325.5	11.0	420	2	T23776	hypothetical prote
40	322	10.8	473	2	T31717	protein M162.5 [im
41	319.5	10.8	452	2	T31101	protein M162.5 [im
42	317	10.7	445	2	D65171	hypothetical prote
43	316	10.6	445	1	T33942	protein ZK652.10 -
44	314	10.6	478	2	T20746	hypothetical prote
45	311.5	10.5	537	2		hypothetical prote

ALIGNMENTS

RESULT 1
I59302
brain specific Na+-dependent inorganic phosphate cotransporter - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I59302
R;Ni, B.; Rosteck, P.R.; Nadi, N.S.; Paul, S.M.
Proc. Natl. Acad. Sci. U.S.A. 91, 5607-5611, 1994
A;Title: Cloning and expression of a cDNA encoding a brain-specific Na(+)-dependent inor
A;Reference number: I59302; MUID:94261635; PMID:8202535
A;Accession: I59302
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-560 <RES>
A;Cross-references: UNIPROT:Q62634; EMBL:U07609; NID:g507414; PIDN:AAA19646.1; PID:g5074

Query Match   98.5%; Score 2925; DB 2; Length 560;
Best Local Similarity 98.2%;
Matches 550; Conservative   5; Mismatches   5; Indels   0; Gaps   0;

```
Qy          1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLBLSADGRPVTTQTRDPPVVDCTCFGLP 60
              ||||||||||||||||||||||:|:||||||||||||||||||||||||||||||||||||
Db          1 MEFRQEEFRKLAGRALGRLHRLLEKRQEGAETLBLSADGRPVTTHTRDPPVVDCTCFGLP 60

Qy         61 RRYIIAIMSGLGFCISFGIRCNLGIVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RRYIIAIMSGLGFCISFGIRCNLGIVAIVSMVNNSTTHRGGHVVVQKAQFNWDPETVGLIH 120

Qy        121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILOG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILOG 180

Qy        181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVSYV 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFV 240

Qy        241 YGSFGIFWYLFWLLVSYBSPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
              ||||||||||||||||||||||||||||||||||||||:|||:||||||||||||||||||
Db        241 YGSFGIFWYLFWLLVSYBSPALHPSISEEERKYIEDAIGESAKLMNPVTKFNTPWRRFFT 300

Qy        301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGQ 360
              |||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        301 SMPVYAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy        361 IADFLRSRRIMSTTNVKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 IADFLRSRHIMSTTNVRKLMNCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy        421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
```

```
Qy  481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
        ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db  481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDESEMEDEVEPPGAPPAPPPS 540

Qy  541 YGATHSTFQPPRPPPPVRDY 560
        ||||||||| |||||||||
Db  541 YGATHSTVQPPRPPPPVRDY 560
```

RESULT 2
H88548
protein ZK512.6 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
A;Accession: H88548
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: H88548
A;Molecule type: DNA
A;Residues: 1-576 <STO>
A;Cross-references: UNIPROT:P34644; GB:chr_III; PIDN:CAA80150.1; PID:g3881690; GSPDB:GNO
C;Genetics:
A;Gene: ZK512.6
A;Map position: 3

```
Query Match        43.7%;   Score 1297;  DB 2;   Length 576;
Best Local Similarity  47.7%;  Pred. No. 3.4e-97;
Matches 262;  Conservative 88;  Mismatches 171;  Indels 28;  Gaps 10;

Qy    9 RKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDP---PVVDCTCFGLPR-RYI 64
        |:| ||||||||||||:|||||||||||||||||||||||    :|| |:|||||| ||:
Db   12 KQMVGEPLAKMTAAAASATGAAPPQQMQEEGNENPMQMHSNKVLQVMEQTWIGKCRKRWL 71

Qy   65 IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFF 124
        :|::..:||.|||||||||.|| :..: ...:  : .|.| |::::::.|:..:::.|.:
Db   72 LAILANMGFMISFGIRCNFGAAKTHMYKNYTDPYG---KVHMHEFNWTIDELSVMESSYF 128

Qy  125 WGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYG-CVIFVRLLQGLVE 183
        :||:||||| ||: .:| .|::|||.|.|.:.|.:|:| |::|:   ||:|.::|||||:
Db  129 YGYLVTQIPAGFLAAKFPPNKLFGFGIGVGAFLNILLPYGFKVKSDYLVAFIQITQGLVQ 188

Qy  184 GVTYPACGIWSKWAPPLERSRLATTAFCGGSYAGAVAVAMPLAGVLVQYSGWSSSVFYVY 243
        || |||.|:|. ||||:|||:||||||.|||||||| . :||:.:||:|.|||:: ||:|
Db  189 GVCYPAMIGVWRYWAPPMERSKLATTAFTGSYAGAVLGLPLSAFLVSYSVSWAAPFYLYG 248

Qy  244 FGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFPTSMP 303
        .|::|.|.|.:.::|||:|||:||:||::.|||||||.:.: : |:::.|||::. ||:|
Db  249 CGVIWALLWFCVTFEKPAFHPTISQEEKIFIEDAIGHVSN-THPTIR-SIPWKAIVTSKP 306

Qy  304 VYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIAD 363
        |:|||||||.|||||||||.|: | .::.:|::|:.:|::|||||||| .:||:|||:||
Db  307 VWAIIVANFARSWTFYLLLQNQLTYMKEALGMKIADSGLLAAIPHLVMGCVVLMGGQLAD 366

Qy  364 FLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVCGYSHSKGVAISFLVLAVGFSFGFAISG 423
        :||| :::|||.|||::||||||.||:::|:|..|:  | .|:.:::.|||.|.|||||.
Db  367 YLRSNKILSTTAVRKIFNCGGFGGEAAFMLIVAYTTSDTTAIMALIAAVGMSGFAISGFN 426

Qy  424 VNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGV 483
        |||||||||||:|||:|||:|||:.|:.||:.. |:|.:  .:.|  ||||||::|:.||
Db  427 VNHLDIAPRYAAILMGFSNGIGTLAGLTCPFVTEAFTAH-SKHGWTSVFLLASLIHFTGV 485

Qy  484 IFYGVFASGEKQPWAEPEEMSE------------EKCGFVG---------HDQLAGSDDSEMEDE 527
        .| .|:||||:|.|||| |:.:            |||||.          ||:||||::|||:|
Db  486 TFVAVYASGELQEWAEPKEEEEWSNKELVNKTGINGTGYGAAETTFTQLPAGVDSSYQAQ 545

Qy  528 AEP-PGAPP 535
        | | ||:.|
Db  546 AAPAPGTNP 554
```

RESULT 3
T43650
probable sodium-dependent inorganic phosphate cotransporter - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
A;Accession: T43650
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
A;Reference number: Z22599
R;Lee, R.Y.N.; Sawin, E.R.; Chalfie, M.; Horvitz, H.R.; Avery, L.
submitted to the EMBL Data Library, September 1998
A;Description: EAT-4, a homolog of a mammalian sodium-dependent inorganic phosphate cotr
A;Reference number:
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-563 <LEE>
A;Cross-references: UNIPROT:Q9TZN7; EMBL:AF095787; PIDN:AAC64972.1
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: eat-4
A;Map position: 3
A;Function:
A;Description: is necessary for glutamatergic neurotransmission

```
Query Match        43.6%;   Score 1294;  DB 2;   Length 563;
Best Local Similarity  47.9%;  Pred. No. 5.8e-97;
Matches 262;  Conservative 86;  Mismatches 171;  Indels 28;  Gaps 10;

Qy   11 LAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDP---PVVDCTCFGLPR-RYIIA 66
        |||||||||||||:|||||||||||||||||||||||    :|| |:|||||| ||::|
Db    1 MVGEPLAKMTAAAASATGAAPPQQMQEEGNENPMQMHSNKVLQVMEQTWIGKCRKRWLLA 60

Qy   67 IMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFFWG 126
        :.:.:||.|||||||||.|| :..: ...:  : .|.| |::::::.|:..:::.|.::|
Db   61 ILANMGFMISFGIRCNFGAAKTHMYKNYTDPYG---KVHMHEFNWTIDELSVMESSYFYG 117

Qy  127 YIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYG-CVIFVRLLQGLVEGV 185
        |:||||| ||: .:| .|::|||.|.|.:.|.:|:| |::|:   ||:|.::|||||:||
Db  118 YLVTQIPAGFLAAKFPPNKLFGFGIGVGAFLNILLPYGFKVKSDYLVAFIQITQGLVQGV 177

Qy  186 TYPACGIWSKWAPPLERSRLATTAFCGGSYAGAVAVAMPLAGVLVQYSGWSSSVFYVYVYGSFG 245
        .|||.|:|. ||||:|||:||||||.|||||||| . :||:.:||:|.|||:: ||:||:.|
Db  178 CYPAMHGVWRYWAPPMERSKLATTAFTGSYAGAVLGLPLSAFLVSYSVSWAAPFYLYGVCG 237

Qy  246 IFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPVV 305
        :.|.|.|.:.::|||:|||:||:||::.|||||||.:.: : |:::.|||::. ||:|:|
Db  238 VIWALLWFCVTFEKPAFHPTISQEEKIFIEDAIGHVSN-THPTIR-SIPWKAIVTSKPVW 295

Qy  306 AIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADFL 365
        |||||||.|||||||||.|: | .::.:|::|:.:|::|||||||| .:||:|||:||:|
Db  296 AIIVANFARSWTFYLLLQNQLTYMKEALGMKIADSGLLAAIPHLVMGCVVLMGGQLADYL 355

Qy  366 RSRRIMSTTNVRKLMNCGGFGMEATLLLVVCGYSHSKGVAISFLVLAVGFSFGFAISGFN 425
        ||| :::|||.|||::||||||.||:::|:|..|:  | .|:.:::.|||.|.|||||.|
Db  356 RSNKILSTTAVRKIFNCGGFGGEAAFMLIVAYTTSDTTAIMALIAAVGMSGFAISGFNVN 415

Qy  426 HLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVIF 485
        ||||||||:|||:|||:|||:.|:.||:.. |:|.:  .:.|  ||||||::|:.||.|
Db  416 HLDIAPRYAAILMGFSNGIGTLAGLTCPFVTEAFTAH-SKHGWTSVFLLASLIHFTGVTF 474

Qy  486 YGVFASGEKQPWAEPEEMSE------------EKCGFVG---------HDQLAGSDDSEMEDEAE 535
        |.|:||||:|.|||| |:.:            |||||.          ||:||||::|||:|||
Db  475 YAVYASGELQEWAEPKEEEEWSNKELVNKTGINGTGYGAAETTFTQLPAGVDSSYQAQAA 534

Qy  530 P-PGAPP 535
        | ||:.|
Db  535 PAPGTNP 541
```

RESULT 4
T23589
hypothetical protein K10G9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans

```
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A;Accession: T23589, T24636
R;Mortimore, B.
submitted to the EMBL Data Library, August 1994
A;Reference number: Z19765
C;Accession: T23589
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-573 <WIL>
A;Cross-references: UNIPROT:Q09932; EMBL:Z36282; PIDN:CAA85289.1; GSPDB:GN000021; CESP:K1
A;Experimental source: clone K10G9
C;Genetics:
A;Gene: CESP:K10G9.1
A;Map position: 3
A;Introns: 38/3; 87/3; 224/1; 272/3; 322/3; 444/3; 476/3; 496/1; 517/2

Query Match        32.7%;  Score 971;  DB 2;  Length 573;
Best Local Similarity  43.5%;  Pred. No. 9.5e-71;
Matches  197;  Conservative  83;  Mismatches 163;  Indels  10;  Gaps  5;

Qy   62 RYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHG 121
Db   47 RWQIALLAHFGFAISFGIRSNFGVAKNRMINNFTDAYG---EVHEREFLWTGAEVGMMES 103

Qy  122 SFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFV--RIL 178
Db  104 SFFYGYVAASQIPAGVLAAKFAPNKLFMLGILFASLINIVTAICLNFHPYTDIFVMVIQVM 163

Qy  179 QGLVEGVTYPACHGIWSKWAPPLERSRLAITTAFCGSYAGAVVAMPLAGVLVQYSGWSSVF 238
Db  164 QGLALGVCYPAMHGVWNKYWAPPLERSKLATTTFTGASVGVWGLPASAYLVSHFSWSTPF 223

Qy  239 YVYGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRF 298
Db  224 YVFGALGIVWSILWIVSGTSPETHGYISADEKKYITEKVGSVA--VKNMTLTTLPWRDM 281

Qy  299 FTSMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIG 358
Db  282 MTSAVWAIIICSFCRSWSFFLLGNQLTYMKDVLIHIDIKNSGLIAIFPQLGMCIVTLTS 341

Qy  359 GQIADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFA 418
Db  342 GQLSDYLRSSGKMSTEAVRKSVNTFGFTVEAVMLGCLAFVRDPVIAVTFLIIACSGAGAV 401

Qy  419 ISGFNVNHLDIAPRYASILMGISNGVGTLSGNVCPIIVGAMTKHKTREEWQYVFLIASLV 478
Db  402 LSGFNVNHFDIAPRHAPILMGIANGLGAIAG--VGGIVTNSLT--YQNPDGWQWVFLLAMSI 459

Qy  479 HYGGVIFYGVPASGEKQPWAEPEEMSEEKCGFV 511
Db  460 DIFGIIFFLIFAKGDVLPWAREPEKEETFNEFV 492
```

RESULT 5

T24633
hypothetical protein T07A5.3 - Caenorhabditis elegans

```
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
A;Introns:
R;Buck, D.
submitted to the EMBL Data Library, February 1995
A;Reference number: Z19915
A;Accession: T24633
A;Status: preliminary; translated from GB/EMBL/DDBJ
```

```
A;Molecule type: DNA
A;Residues: 1-544 <WIL>
A;Cross-references: UNIPROT:Q10046; EMBL:Z48055; PIDN:CAA88134.1; GSPDB:GN000021; CESP:T0
A;Experimental source: clone T07A5
C;Genetics:
A;Gene: CESP:T07A5.3
A;Map position: 3
A;Introns: 38/3; 87/3; 272/3; 322/3; 444/3; 476/3; 496/1; 517/2

Query Match        32.0%;  Score 950;  DB 2;  Length 544;
Best Local Similarity  41.4%;  Pred. No. 4.5e-69;
Matches  208;  Conservative  78;  Mismatches 171;  Indels  46;  Gaps  9;

Qy   62 RYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHG 121
Db   47 RWQIALLAHFGFAISFGIRSNFGVAKNRMVNNFTDAYG---EVHEREFLWTGAEVGMMES 103

Qy  122 SFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFV--L 178
Db  104 SFFYGYVAASQIPAGVLAAKFAPNKIFMLGILVASFMNILSAISFNFHPYTDIFVMVVQAV 163

Qy  179 QGLVEGVTYPACHGIWSKWAPPLERSRLAITTAFCGSYAGAVVAMPLAGVLVQYSGWSSVF 238
Db  164 QGLALGVLYPAMHGVWKFWAPPLERSKLATTTFTGSSVGVWTGLPASAYLVSHFSWSTPF 223

Qy  239 YVYGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRF 298
Db  224 YVFGVVGIIWSLIWMYVSSHSPETHGYISDDEKKVQVTEKIGDVAVKNMSLT--TLPWRDM 281

Qy  299 FTSMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIG 358
Db  282 MTSSAVWAIIICTFCRSWGFFLLLGNQLTYMKDVLHIDIKNSGFISIFPQFGMCIVTLAT 341

Qy  359 GQIADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFA 418
Db  342 GQLCDYLRSSGKMSTEAVRKSVNTFGFTVEAVMLGCLAFVRDPVIAVTCLVIACTGSGSV 401

Qy  419 ISGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAM------TKHKTREEWQYVFLI 474
Db  402 LSGFNVNHFDIAPRYAPILMGIANGLGAVAG-----VGGMVTNTVTYQNPDGWKWVFLL 455

Qy  475 ASLVHYGGVIFYGVFASGEKQPWA-EPEE------MSEEKCGFVGH 513
Db  456 AMAIDIFGVIFFLIFAKGDVLPWAREPEKEETFNEFVRRMSIKVRSLSRKTRNREGDTSY 515

Qy  514 DQLAGSDDSEMED-------EAEPP 531
Db  516 EKN--EEDSEMKPCSKKVEARAP 536
```

RESULT 6

S40767
hypothetical protein ZK512.6 - Caenorhabditis elegans

```
C;Species: Caenorhabditis elegans
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
A;Accession: S40767
R;Hawkins, T.; Ainscough, R.
submitted to the EMBL Data Library, February 1993
A;Reference number: S40759
A;Accession: S40767
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-466 <HAM>
A;Molecule type: DNA
A;Cross-references: UNIPROT:P34644; EMBL:Z22177
C;Genetics:
A;Introns: 21/2; 38/2; 109/3; 149/2; 188/3; 247/1; 292/3; 346/1; 376/3; 451/2
C;Keywords: transmembrane protein

Query Match        29.8%;  Score 885;  DB 2;  Length 466;
Best Local Similarity  41.7%;  Pred. No. 6.9e-64;
Matches  185;  Conservative  75;  Mismatches 140;  Indels  44;  Gaps  8;

Qy    9 RKLAGRALGKLHRLLEKROEGAETLELSADGRPVTTQTRDP---PVVDCTCFGLPR-RYI 64
```

```
Db     12 KQMVGEPLAKMTAAAASATGAAPPQOMOBEGNGNENPMQMHSNKVLQVMEQTWIGKCRKRWL 71
             :::       ||:      |:::|     |||       |||:
Qy     65 IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFF 124
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     72 LAILAANMGFMISFGIRCNFGAAKTHMYXKNYTDPYG---KVHMHEFNWTIDELSVMESSYF 128

Qy    125 WGYIVTVQIPGGFICQKFPAANRVPGFAIVATSTLNMLIPSAARVHYG-CVIFVRILQGLVE 183
          :||:|||||||||||||||||||||||||||||||||||||||||:::||:|||||:||
Db    129 YGYLVTQIPAGFLAAKFPPNKLPGFGFGIGVGAFLNILLPYGFGFKVKSDVLVAFIQITQGLVQ 188

Qy    184 GVTYPACHGIWSKWAPLLERSRLATTAFCGSYAGAVAMPLAGVLVQYSGWSSVFYVYGS 243
          :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 GVCYPAMIGVWRYWAPPMERSKLATTAFTGSYAGAVGLPLSAFLVSTVTVSWAAPFYLLGV 248

Qy    244 FGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESSAKLMNPLTKFSTPWRRFFTSMP 303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249 CGVIWAILMFCVTFEKPAFHPTISQEEKIFIEDAIGHVSN-THP-TLFLLAYFNFFLEP 306

Qy    304 ------------------------VTAIIV------------ANFCRSWTFYLLLISQPDYF 329
                                    ||:|         :|:
Db    307 AKVTQNTMLLENFGIYQNFANLQKLIISVNNPAPKINNKFANFARSWTFYLLLQNQLTYM 366

Qy    330 EEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADFLRSRRIMSTTNVRKLMNCGFGMEA 389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 KEALGMKIADSGLIAAIPHLVMGCVTLMGGQLADYLRSNKILSTTAVRKIFNCGGFGGEA 426

Qy    390 TLLLVVGYSHSKGVAISFVLAVG 413
          :|::|||||||||||||||||||
Db    427 AFMLIVAYTISDTTAIMALIAAVG 450
```

RESULT 7
G88553
protein C38C10.2 [imported] - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G88553
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: G88553
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-493 <STO>
A;Cross-references: UNIPROT:Q03567; GB:chr_III; PIDN:CAA79549.1; PID:g3874873; GSPDB:GN0
C;Genetics:
A;Gene: C38C10.2
A;Map position: 3

Query Match 26.1%; Score 775.5; DB 2; Length 493;
Best Local Similarity 32.3%; Pred. No. 5.6e-55;
Matches 163; Conservative 102; Mismatches 196; Indels 43; Gaps 9;

```
Qy     46 TRDPPVVDCTCFGLPRRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQ 105
             |:|                |:|||||||||||||||||||||||||||||||||||||
Db      5 TTKPRLVPST-----RFALSLVMFPGCLVTYMMRTNMSFAVVCMVNENKTDTG----VE 54

Qy    106 K---------------AQFSWDPETVGLIHGSFFWGYIVTVQIPGGFICQKFPAANRVF 147
                           |||||||||||||||||||||||||||||||||||||||||||
Db     55 KVSRCGKEMTPVESNSSVIGEFDWDKQTTGMVLSSFFYGYIGSQIIGHLASRYGGKRVV 114

Qy    148 GFAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEGVTYPACHGIWSKWAPPLERSRLA 207
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    115 FVTILGSALLTLLNPVAARTSEYALALRAAIGFLQGATFPAMHTMWSVWGPPLELSVLT 174

Qy    208 TTAFCGSYAGAVAMPLAGVLVQY---------SGWSSVFYVYGSFGIFWYLFWLLVSYESPALHP 264
          |:|                      ||||||||||||||||||||||||||||||||||||||||
Db    175 GVTYAGAQIGNVIVLPLSGFLCEYGFDGGWPSIFYIIGVFGVLWTAVWWNYVSSDKPATHP 234
```

C;Species: Caenorhabditis elegans
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 16-Feb-1997
C;Accession: S28286
R;Thomas, K.
submitted to the EMBL Data Library, December 1992
A;Reference number: S28285
A;Accession: S28286
A;Molecule type: DNA
A;Residues: 1-472 <THO>
A;Cross-references: EMBL:Z19153
C;Genetics:
A;Genetics:
A;Introns: 50/3; 287/3; 351/3; 412/3
A;Introns: 51/3; 412/3
C;Keywords: transmembrane protein

Query Match 25.7%; Score 763.5; DB 2; Length 472;
Best Local Similarity 33.1%; Pred. No. 5e-54;
Matches 158; Conservative 96; Mismatches 187; Indels 37; Gaps 8;

```
Qy    265 SISEEERKYIEDAIGESSAKLMNPLTKF-STPWRRFFTSMPVYAIIVANFCRSWTFYLLLI 323
          ||||||||||||||||||||||||||    :|||||||||||||:|:|||||||||||||
Db    235 RITPEEKQYIVTAV--EASMGKDTGKVPSTPWIKILTSPAVWACWAGHIFAGDWGAYTMLV 292

Qy    324 SQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADFLRSRRIMSTTNVRKLMNCG 383
          :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    293 SLFSFLKDVLGLNLSSLGAVASIPYIAYFLAINAGGVLADTLRSKGILSTLNTRRAAMLV 352

Qy    384 GFGMEATLLLVVGY--SHSKGVAISFVLAVGRSGFAISGFNVNHLDIAPRYASILMGIS 441
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    353 ALIGQGIFLVASGYCGCGQDVLVIFITCGMAISGLQYAGFVVNYLEIAPFFSGTVMGTG 412

Qy    442 NGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLLIASLVHYGGVIFYGVFASGEKQPWAEPE 501
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    413 NTISALAGIISPAVSSYLTPNGTQEEWQMVLWLTAGILITIGALLFSIFASGEVQPWA--- 469

Qy    502 EMSEEKCGFVGHDQLAGSDDSEME 525
          :||||||||||||||||||||||:
Db    470 KLITAEE------GHEMAPLREGEKIE 489
```

RESULT 9

H84698
hypothetical protein At2g29650 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H84698
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
Nature 402, 761-768, 1999
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84698
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-512 <STO>
C;Cross-references: UNIPROT:O82390; GB:AE002093; NID:g3582333; PIDN:AAC35230.1; GSPDB:GN
C;Genetics:
A;Gene: At2g29650
A;Map position: 2
C;Superfamily: hexuronate transporter

Query Match   24.3%; Score 720.5; DB 2; Length 512;
Best Local Similarity   35.9%; Pred. No. 1.7e-50;
Matches 157; Conservative 71; Mismatches 180; Indels 29; Gaps   5;

```
Qy  60 PRRYIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQPSWDPETVGLI 119
Db 100 PKRWIVLLCFSAFLLCMDRVNMSIAILPM----------SAEYGWNPATVGLI 144

Qy 120 HGSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQ 179
Db 145 QSSFFWGYLLTQIAGGIWADTVGGKRVLGFGVIWSIATILTPVAAKLGLPYLLVVRAFM 204

Qy 180 GLVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVAVAMPLAGVLVQYSGWSSVFY 239
Db 205 GVGEGVAMPANNNILSKWVPVQERSRSLALVYSGMYLGSVTGLAFSPFLIHQFGWPSVFY 264

Qy 240 VYGSFGIFWLFWLLVSYESPALHPSISEEERKYIED--AIGESAKLMNPLTKFSTPWRR 297
Db 265 SFGSLGTVWLTLWLRXAESSPLEDPTLPEERKLIADNCASKEPVK------SIPWRL 316

Qy 298 FFTSMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPI 357
Db 317 ILSKPPVWALISCHFCHNWGTFILLITWMPIYTYHQVLKFNLMESGLLSVFPMMTMAISANA 376

Qy 358 GGQIADFLRSRRIMGTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGF 417
Db 377 GGWIADTLVSRG--FSVTNVRKIMQTIGFLGPAFFLTQLKHIDSPTMAVLCMACSQGTDAF 435

Qy 418 AISGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASL 477
Db 436 SQSGLYSNHQDIAPRYSGVLLGLSNTAGVLAGVLGTAAATGHILQHGS---WDDVFFISVG 492

Qy 478 VHYGGVIFYGVFASGEK 494
Db 493 LYLVGTVIWNLFSTGEK 509
```

RESULT 10

A56410
sodium/phosphate transport protein, renal - rabbit
N;Alternate names: sodium/phosphate cotransporter
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: A56410; S27951
R;Werner, A.; Moore, M.L.; Mantei, N.; Biber, J.; Semenza, G.; Murer, H.
Proc. Natl. Acad. Sci. U.S.A. 88, 9608-9612, 1991
A;Title: Cloning and expression of cDNA for a Na/P-i cotransport system of kidney cortex
A;Reference number: A56410; MUID:92052140; PMID:1946375
A;Accession: A56410
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-465 <WER>
A;Cross-references: UNIPROT:Q27722; GB:M76466; NID:g165689; PIDN:AAA31461.1; PID:g165690
A;Keywords: kidney; transmembrane protein

Query Match   23.1%; Score 685.5; DB 2; Length 465;
Best Local Similarity   32.5%; Pred. No. 1e-47;
Matches 152; Conservative 89; Mismatches 190; Indels 37; Gaps   9;

```
Qy  54 CTCFGLPRRYIAIMSGLGFC--ISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQK----- 106
Db  12 CFC---SPRYVLALF--MHFCNIVIIAQRMCLSLTMVAMVNTNLHGSPNTSAEKRLDNT 66

Qy 107 --AQFSWDPETVGLIHGSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSA 164
Db  67 KNPVYNWSPDVQGIIFESSIFYGAFLIQIPVGYISGIYSIKKLLIGPALFLSSLVSIFIPQA 126

Qy 165 ARVHYGCVIFVRILQGLVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVAVAMPL 224
Db 127 AAVGEBTWIIVCRVWQGIIQGTVVTTAQHHIWVKWAPPLERGRLTSMSLSGFLLGPFIVLLV 186

Qy 225 AGVLVQYSGWSSVFYVYVGSFGIFWLFWLLVSYESPALHPSISEEERKYIEDAI--GBS 281
Db 187 TGIICESLGWPMWFYIFGACGCAVCLLWFVLYDDPKDHPCVSLHEKEYITSSLIQGSS 246

Qy 282 AKLMNPLTKFSTPWRRFFTSMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVG 341
Db 247 -----TRQSLPIKAMIKSLPLWAISFCCFAYLWTSRLIVYTPTLLINSMLHVDIRENG 299

Qy 342 LVSALPHLVMTIIVPIGGQIADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLLVVGYSH-- 399
Db 300 LLSSLPYLFAWICGVIAGHTADFLMSRNMLSTIARIKLFTAIG-----LLLPIVFSMCL 353

Qy 400 --SKGV--AISFLVLAVGFSGGFPAISGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPI 454
Db 354 LYLSSGFYSTIFFLILANASSSFCLGGALINALDLARYYVFIKGVTTLIGWTGGMTSST 413

Qy 455 IVGAMTKHKTREEWQYVFLIASLVHYGGVIFYGVFASGEKQPWAEPEE 502
Db 414 VAGLFLSQDPESSWFKIFLLMSIINVISVIFLYLIFAKAEIQDWAKEKQ 461
```

RESULT 11

A48916
sodium phosphate transport protein 1, renal - human
C;Species: Homo sapiens (man)
A;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C;Accession: A48916
R;Chong, S.S.; Kristjansson, K.; Zoghbi, H.Y.; Hughes, M.R.
Genomics 18, 355-359, 1993
A;Title: Molecular cloning of the cDNA encoding a human renal sodium phosphate transport
A;Reference number: A48916; MUID:94117004; PMID:8288239
A;Accession: A48916
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-467 <CHO>
C;Cross-references: GB:X71355; NID:g450531; PIDN:CAA50490.1; PID:g450532
C;Genetics:
A;Gene: GDB:141889; NPT1
A;Cross-references: GDB:141889; OMIM:182308
A;Map position: 6p23-6p21.3

Query Match   21.1%; Score 626.5; DB 2; Length 467;
Best Local Similarity   30.0%; Pred. No. 6.4e-43;
Matches 136; Conservative 94; Mismatches 197; Indels 27; Gaps   5;

```
Qy  72 GFC---ISFGIRC---------NLGVAIVSMVNNSTTHRGGHVVVQK-----AQF 109
Db  14 GFCSFRYGLSFLVHCCNVIITAQRACLNLTMVVMVNSTDPHGLPNTSTKKLLDNIKNPMY 73

Qy 110 SWDPETVGLIHGSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHY 169
```

RESULT 12

S69915

sodium-phosphate transport system 1 - mouse

C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S69915
R;Chong, S.S.; Kozak, C.A.; Liu, L.; Kristjansson, K.; Dunn, S.T.; Bourdeau, J.E.; Hughe
Am. J. Physiol. 268, 1038-1045, 1995
A;Title: Cloning, genetic mapping, and expression analysis of a mouse renal sodium-depen
A;Accession: S69915
A;Reference number: S69915
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-465 <CHO>
A;Cross-references: UNIPROT:Q61983; EMBL:X77241; NID:g887522; PIDN:CAA54459.1; PID:g8875

Query Match   20.8%; Score 619; DB 2; Length 465;
Best Local Similarity   31.5%; Pred. No. 2.6e-42;
Matches 141; Conservative 88; Mismatches 203; Indels 16; Gaps   6;

```
Qy     74 NWSPDIQGTILSSTSYGVTIIQVPVGYPSGIYSTKKMIGFALCLSSVLSLLIPPAAGIGV 133
          |:|||:| |||||: :  | |::|||:|||  |:||||||:::: ||| ||
Db    371 NSTLSFSYCGQLINALDIAPRYGFLKAVTALIGMFGGGLISSTLLAGLILNQDPEYAWHKI 430

Qy    170 GCVIFVRILQGLIVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVAVAMPLAGVLV 229
          ||||| :::|:| ::| :| || |: |||| ::::  :  |:::|| :|  ||
Db    472 FLIASLVHYGGVIFYGVFASGEKQPWAE 499

Qy    134 AWVVVCRAVQGAAQGIVATAQFEIYVKWAPPLERGRLITSMSTSGFLLGPFIVLLVTGVIC 193
          ::  :| : :| :||  |:|| :||  ||:| | :::::|:||:  |:|| | || :|
Db    431 SFLMAGINVTCLIVFYFLFPAKGEIQDWAK 458

RESULT 13

I39473

Na+-dependent phosphate cotransporter - human

C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I39473
R;Miyamoto, K.; Tatsumi, S.; Sonoda, T.; Yamamoto, H.; Minami, H.; Taketani, Y.; Takeda,
Biochem. J. 305, 81-85, 1995
A;Title: Cloning and functional expression of a Na(+)-dependent phosphate co-transporter
A;Accession: I39473
A;Reference number: I39473; MUID:95126933; PMID:7826357
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-465 <RES>
A;Cross-references: UNIPROT:Q14916; GB:D28532; NID:g639841; PIDN:BAA05888.1; PID:g639842

Query Match         20.8%;  Score 616.5;  DB 2;  Length 465;
Best Local Similarity   29.7%;  Pred. No. 4.1e-42;
Matches  135;  Conservative  94;  Mismatches 198;  Indels  27;  Gaps   5;

Qy     74 NWSPDIQGTILSSTSYGVTIIQVPVGYPSGIYSTKKMIGFALCLSSVLSLLIPPAAGIGV 131
          |:|||:| |||||: :  | |::|||:|||  |:|||||||:::: ||| ||
Db     72 NWSPDVQGTILSSTSYGVIIIQVPVGYFSGIYSTKKMIGFALCLSSVLSLLIPPAAGIGV 131

Qy    132 AWVVVCRAVQGAAQGIVATAQFEIYVKWAPPLERGRLITSMSTSGFLLGPFIVLLVTGVIC 191
          :| | |: :|  :| | |: ::| |:||  :::| : :|:| |:  |:||  ||| : ||
Db    132 AWVVVCRAVQGAAQGIVATAQFEIYVKWAPPLERGRLITSMSTSGFLLGPFIVLLVTGVIC 191

Qy     72 GFC------ISFGIRC------------NLGVAIVSMVNNSTTHRGGHVVVQK------AQF 109
          |||      ||||||             |||||| |:  ::|:::  |  |::      |:|
Db     12 GFCSFRYGLSFLVHCCNVIITAQLMCLNLTMVVWNSTDPGHLPNTSTKLLDNIKNPMY 71

Qy    110 SWDPETVGLIHGSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHY 169
          | |||||||| ||  ||| |:|| |||  ||||||:||||| |:: ||: ||| :|  |
Db     12 GFCSFRYGLSFLVHCCNVIITAQLMCLNLTMVVWNSTDPGHLPNTSTKLLDNIKNPMY 71

Qy    170 GCVIFVRILQGLIVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVAVAMPLAGVLV 229
          ||||| :::|:| ::| :| || |: |||| ::::  :  |:::|| :|  || ||||:| |
Db    170 GCVIFVRILQGLIVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVAVAMPLAGVLV 229

Qy    230 QYSGWSSVFYVYGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLIT 289
          |||||:||||||||||||||||||||||||:||:||| |||| |||| ||| |:|:||:||
Db    132 AWVVVCRAVQGAAQGIVATAQFEIYVKWAPPLERGRLITSMSTSGFLLGPFIVLLVTGVIC 191

Qy    230 QYSGWSSVFYVYGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLIT 289
          |||||:||||||||||||||||||||||||:||:||| |||| |||| ||| |:|:||:||
Db    230 QYSGWSSVFYVYGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLIT 289

Qy    290 KFSTPWRRFFTSMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHL 349
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    290 KFSTPWRRFFTSMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHL 349

Qy    350 VMTIIVPIGGQIADFLRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAI-SFL 408
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| :|||
Db    350 VMTIIVPIGGQIADFLRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAI-SFL 408

Qy    409 VLAVGFSGGFAISGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEW 468
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    368 ILAGATGSFCLGGVFINGLDIAPRYFGFIKACSTLTGMIGGLIASTLTGLILIKQDPESAW 427

Qy    469 QYVFLIASLVHYGGVIFYGVFASGEKQPWAEPEE 502
          ||||||||||||||||||||||||||||||||||
Db    428 FKTFILMAAINVTGLIFYLIVATAEIQDWAKEKQ 461

RESULT 14

T01534

hypothetical protein A_IG005I10.nn - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01534
R;Andrews, S.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of A. thaliana IG005I10.
A;Accession: T01534
A;Reference number: Z14347
A;Molecule type: DNA
A;Status: translated from GB/EMBL/DDBJ
```

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A;Residues: 1-413 <AND>
A;Cross-references: UNIPROT:O23065; EMBL:AF013293; NID:g2252823; PID:g2252847
A;Experimental source: cultivar Columbia
C;Genetic:
A;Map position: 4
A;Introns: 79/3; 115/3; 128/3; 200/3; 288/3; 331/3; 353/3; 382/1
A;Note: A_IG005I10.nn
C;Superfamily: hexuronate transporter

Query Match
Best Local Similarity   20.1%;   Score 596.5;   DB 2;   Length 413;
                        30.7%;   Pred. No. 1.5e-40;
Matches 139;   Conservative 62;   Mismatches 133;   Indels 119;   Gaps 9;

Qy   60 PRRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFS 109
         |||| |  | :||||:||| |:||||:|    ||       ::   |:
Db   59 PRRWIVLLCFSSFLLCNMDRVMSIAILPM---------SQEYNWSSATVGLI 103

Qy  120 HGSFFNGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYG 169
         | :||:| || :    |  :  |   :  :  ||: |||||||:||| |||
Db  104 QSSFFWGYLLTQILGGIWADKFGG------------------------SAV 127

Qy  180 GLVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQ 229
         |:: |:|||| |||||||||||||||||||||||||||||||||||||| :
Db  128 ---KGVAMPAMNMLSKWIPVSERSRSLALVYSGMYLGSVTGLAFSPMLITKFGWPSVFY 184

Qy  240 VYGSFGIFWYLFWLLVSYESSPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFF 299
         |:|||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db  185 SFGSLGSIWFLLWLKPAYSSPKDDDPDLSEEEKKVI--LGGS-KPREPVTVT--PWKLIL 238

Qy  300 TSMPVYAIIVANFCRSWTFYLLLISQPDYF--------EEVFGFEISKVG 341
         |::|:||:|||||||||||||||||||||||        ||:|||||| |
Db  239 SKPPVWALIISHFCHNWGTFILLTWMPTYYNQARSSASVISLLFNIFCEQVLKFNLTESG 298

Qy  342 LVSALPHILVMTIIVPIGGQIADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSK 401
         |:||||||:|| ::::|||||||||||||||||||||||||||||||||||||||||||||
Db  299 LLCVLPWLTMAVFANIGGWIADTLVSRG-LSITN-------------------------331

Qy  402 GVAISFLVLAVGFSGFAISGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTK 461
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db  332 --------GSDAFSQSGLYSNHQDIGPRYAGVLLGLSNTAGVLAGVFGGTAATGYILQ 380

Qy  462 HKTREEWQYVFLIASLVHYGGVIFYGVFASGEK 494
         | ||| ||||||||||||||||||||||||||
Db  381 ---RGSWDDVFKVAVALYLIGTLVWNLFATGEK 410
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```
RESULT 15
T45634
hypothetical protein F13I12.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45634
R;Choine, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa...
submitted to the Protein Sequence Database, November 1999
A;Reference number: Z23010
A;Accession: T45634
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-537 <CHO>
A;Cross-references: UNIPROT:Q9SD75; EMBL:AL133292
A;Experimental source: cultivar Columbia; BAC clone F13I12
C;Genetics:
A;Map position: 3
A;Introns: 35/2; 153/3; 229/2; 350/3; 399/3; 445/3; 457/1
A;Note: F13I12.30

Query Match
Best Local Similarity   15.9%;   Score 471;   DB 2;   Length 537;
                        27.8%;   Pred. No. 3.1e-30;
Matches 141;   Conservative 80;   Mismatches 221;   Indels 66;   Gaps 12;

Qy   51 VVDCTCFGLPRRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFS 110
          |:   ||| |:|  |:| :||||:||| |:||||:|    ||       ::   |:|
Db  102 FSB---FITSERVKVVAMLALALALCNADRVVMSVAIVPL-----SLSRG---------143

Qy  111 WDPETVGLIHGSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYG 170
          :||   | | |::|:| |::|    |  : |   :  :: ||:: |||||||:|:  ||
Db  144 WSKSFSGIVQSSFLWGYLLISPIAGGTLVDRYGGKVVWAWGVALWSLATFLTPWAADSSLW 203

Qy  171 CVIFVRILQGLVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQ 230
          |: ::  ||:: |:|||| |||||||||||||||||||||||||||||||||||||| :
Db  204 ALLAARAWGVABGVALPCMNNMVARWFPPTERSRAVGIAMAGFQGLGNVVGLMLSPILMS 263

Qy  231 YSGWSSVVFYVVCGSFGIFWYLFWLLVSYESSPALHPSISEEERKYIED----AIGESAKLMN 286
          |||:||:||:| ||||||||||||||||||||||||||||||||||||    |||||||||
Db  264 QCGIYGPVIFGLSGFLWLLIVWLSATSSAPDRHPQITKSELEYIKQKKQISTMENKRIS- 322

Qy  287 PLTKFSTPWRRFFTSMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSAL 346
          |::||||||||| |::|:||:|||||||||||||||||||||| ||:|||||| ||||:|
Db  323 --TSGIPPFGRLLSKMPTWAVIVANSMHSWVYHVNL--KQAAWF------------------SAV 365

Qy  347 PHLVMTIIVPIGGQIADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGYAIS 406
          |::|| ::::|||||||||||||||||||||||||||||||||||||||||||||:||
Db  366 PWSMMAFTGYILAGFWSDLL-IRRGTSITLTRKIMQSICFGIPGPGIALIGLTTAKQPLVASA 424

Qy  407 FLVLAVGFSGFAISGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTRE 466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db  425 WLSLAVGLKSFSHLGFLINLQEIAPEYSGVLHGMCLTRAGTLAAIVG--TVGAGFFVELLG 482

Qy  467 EWQYVFLIASLVHYGGVIFYGVFASGEK 494
          ||||||||||||||||||||||||||||
Db  483 SFQGFILLTAILYLLSALFYNIYATGER 510
```

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Search completed: June   2, 2005, 11:32:25
Job time : 44 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2005, 11:19:52 ; Search time 178 Seconds
                                           (without alignments)
                                           1611.036 Million cell updates/sec

Title: US-10-734-731-4 .
Perfect Score: 2970
Sequence: 1 MEFRQEEFRKLAGRALGKLH..............YGATHSTFQPPRPEPPVRDY 560

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_03:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	2962	99.7	560	2	Q9P2U7	homo sapien
2	2953	99.4	560	2	Q6PCD0	homo sapien
3	2925	98.5	560	2	Q62634	rattus norv
4	2460	82.3	576	2	Q6INC8	rattus norv
5	2444	82.8	576	2	Q71SL3	xenopus lae
6	2338.5	78.7	584	2	Q71SL3	xenopus lae
7	2317.5	78.0	582	2	Q8AW47	brachydanio
8	2313	77.9	582	2	Q8AW47	brachydanio
9	2313	77.9	582	2	Q9P2U8	homo sapien
10	2308.5	77.7	582	2	Q20B7	mus musculu
11	2198	74.0	588	2	Q9JI12	rattus norv
12	2198	74.0	588	2	Q8BLE7	mus musculu
13	2198	73.6	589	2	Q8KIQ1	rattus norv
14	2185	72.5	601	2	Q7TSF2	rattus norv
15	2154.5	70.9	601	2	Q8NDX2	homo sapien
16	2107	70.9	402	2	Q8BFU8	mus musculu
17	1981	66.7	515	2	Q7TQH3	mus musculu
18	1358	45.7	592	2	Q8JFT2	brachydanio
19	1297	43.7	576	2	Q7Q3R3	anopheles g
20	1295.5	43.6	632	2	YQQ6_CAEEL	
21	1294	43.6	563	2	P34644	caenorhabdi
22	1198.5	40.4	560	2	Q86P76	drosophila
23	1051	35.4	201	2	Q9TZN7	caenorhabdi
24	1020	34.3	544	2	Q9VQC0	drosophila
25	986.5	33.2	502	2	Q8JZR7	mus musculu
26	971	32.7	573	2	Q7Q580	anopheles g
27	950	32.0	560	2	Q9VDM0	drosophila
28	950	31.6	544	1	YRT3_CAEEL	
29	940	31.6	495	1	S175_HUMAN	
30	931	31.3	495	1	S175_SHEEP	
31	929	31.3	476	2	Q9mzdl	ovis aries
32	929	31.2	495	1	Q7Q579	anopheles g
33	927	31.2	495	1	S175_MOUSE	
34	842	28.4	479	2	Q23514	caenorhabdi

32	798	26.9	533	2	Q9P2U7	homo sapien
33	798	26.9	533	2	Q9VVG7	drosophila
34	787	26.5	559	2	Q70367	anopheles g
35	775.5	26.1	493	1	YLD2_CAEEL	
36	774.5	26.1	493	1	Q3567	caenorhabdi
37	767.5	25.8	535	2	Q7PWK4	anopheles g
38	749	25.2	529	1	PICO_DROME	drosophila
39	747	25.2	483	1	PICO_DROAN	drosophila
40	743.5	25.0	541	2	Q9VR44	drosophila
41	742.5	25.0	591	2	Q8GX78	arabidopsis
42	727.5	24.5	485	2	Q652N5	oryza sativ
43	723.5	24.4	505	2	Q7PSC6	anopheles g
43	723.5	24.4	529	2	Q7QA73	anopheles g
44	723.5	24.4	529	2	Q9SDI4	oryza sativ
45	720.5	24.3	512	2	Q82390	arabidopsis

ALIGNMENTS

RESULT 1
ID   Q9P2U7   PRELIMINARY;   PRT;   560 AA.
AC   Q9P2U7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Brain-specific Na-dependent inorganic phosphate cotransporter.
GN   Name=BNPI;
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=20281869; PubMed=10820226;
RA   Aihara Y., Mashima H., Onda H., Hisano S., Kasuya H., Hori T.,
RA   Yamada S., Tomura H., Yamada Y., Inoue I., Kojima I., Takeda J.;
RT   "Molecular cloning of a novel brain-type Na(+)-dependent inorganic
RT   phosphate cotransporter.";
RL   J. Neurochem. 74:2622-2625(2000).
DR   EMBL; AB032436; BAA92875.1; -.
DR   Genew; HGNC:16704; SLC17A7.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0015321; F:sodium-dependent phosphate transporter acti...; TAS.
DR   GO; GO:0008817; P:phosphate transport; TAS.
DR   InterPro; IPR007114; MFS.
DR   PROSITE; PS50850; MFS; 1.
SQ   SEQUENCE   560 AA;   61613 MW;   C88DAFB34B6E45B6 CRC64;

Query Match   99.7%; Score 2962; DB 2; Length 560;
Best Local Similarity   99.8%;
Matches 559; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTTRDPPVVDCTCFGLP 60
              | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTTRDPPVVDCTCFGLP 60

Qy   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120

Qy   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300

RESULT 2

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Q6PCD0
ID   Q6PCD0      PRELIMINARY;    PRT;   560 AA.
AC   Q6PCD0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Solute carrier family 17, member 7.
GN   Name=SLC17A7;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
DR   EMBL; BC059379; AAH59379.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR007114; MFS.
DR   PROSITE; PS50850; MFS; 1.
SQ   SEQUENCE   560 AA;  61672 MW;  928C45B02B65B45B5 CRC64;
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Query Match 99.4%; Score 2953; DB 2; Length 560;

Best Local Similarity 99.6%; Pred. No. 9.1e-214;
Matches 558; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDDPPVVDCTCFGLP   60
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Db    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDDPPVVDCTCFGLP   60

Qy   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH  120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH  120

Qy  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG  180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVARSTLNMLIPSAARVHYGCVIFVRILQG  180

Qy  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV  240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV  240

Qy  241 YGSFGIFWLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT   300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 YGSFGIFWLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT   300

Qy  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ  360
        |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db  301 SMPVYAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ  360

Qy  361 IADFLRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS  420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 IADFLRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS  420

Qy  421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY  480

Qy  481 GGVIFYGVPASGEKQPWAEPEEMSEEKCCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GGVIFYGVPASGEKQPWAEPEEMSEEKCCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540

Qy  541 YGATHSTFQPPRPPPPVRDY 560
        ||||||||||||||||||||
Db  541 YGATHSTFQPPRPPPPVRDY 560
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RESULT 3

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Q62634
ID   Q62634      PRELIMINARY;    PRT;   560 AA.
AC   Q62634;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Brain specific Na+-dependent inorganic phosphate cotransporter.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ni B., Rosteck P.R., Nadi N.S., Paul S.M.;
RX   MEDLINE=94261635; PubMed=8202535;
RT   "Cloning and expression of a cDNA encoding a brain-specific Na(+)-
RT   dependent inorganic phosphate cotransporter.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:5607-5611(1994).
DR   EMBL; U07609; AAA19646.1; -.
DR   PIR; I59302; I59302.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR007114; MFS.
DR   PROSITE; PS50850; MFS; 1.
SQ   SEQUENCE   560 AA;  61665 MW;  F686809F60GB8305 CRC64;
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Query Match 98.5%; Score 2925; DB 2; Length 560;

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Qy    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDDPPVVDCTCFGLP   60
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Db    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDDPPVVDCTCFGLP   60

Qy   61 RRYIIAIMSGLGFCISFGTRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RRYIIAIMSGLGFCISFGTRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH  120

Qy  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVARSTLNMLIPSAARVHYGCVIFVRILQG  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVARSTLNMLIPSAARVHYGCVIFVRILQG  180

Qy  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFVV  240

Qy  241 YGSFGIFWLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT   300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 YGSFGIFWLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT   300

Qy  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ  360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ  360

Qy  361 IADFLRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS  420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 IADFLRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS  420

Qy  421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY  480
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Db  421 GFNVNHLDIARRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY  480

Qy  481 GGVIFYGVPASGEKQPWAEPEEMSEEKCCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GGVIFYGVPASGEKQPWAEPEEMSEEKCCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540

Qy  541 YGATHSTFQPPRPPPPVRDY 560
        ||||||||||||||||||||
Db  541 YGATHSTFQPPRPPPPVRDY 560
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Best Local Similarity 98.2%; Pred. No. 1.2e-211;
Matches 550; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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Qy      1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
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Db      1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTHTRDPPVVDCTCFGLP 60

Qy     61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
          ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db     61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFNWDPETVGLIH 120

Qy    121 GSFFWGYIVTQIPGGFICQKFAANRVPGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GSFFWGYIVTQIPGGFICQKFAANRVPGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy    181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy    241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300

Qy    301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy    361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
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Db    361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy    421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
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Db    421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy    481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
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Db    481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDESEMEDEVEPPGAPPAPPPS 540

Qy    541 YGATHSTFQPPRPPPPVRDY 560
          ||||||||:||||||||||
Db    541 YGATHSTVQPPRPPPPVRDY 560
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RESULT 4
Q6INC8

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ID    Q6INC8              PRELIMINARY;    PRT;    576 AA.
AC    Q6INC8;
DT    05-JUL-2004 (TrEMBLrel. 27, Created)
DT    05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT    05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE    MGC83509 protein.
GN    Name=MGC83509;
OS    Xenopus laevis (African clawed frog).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC    Xenopodinae; Xenopus.
OX    NCBI_TaxID=8355;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    TISSUE=Eye;
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RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RA   Klein S., Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC072355; AAH72355.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR007114; MFS.
DR   PROSITE; PS50850; MFS; 1.
SQ   SEQUENCE   576 AA;   63905 MW;   93C2157CFB15CB62 CRC64;

Query Match   82.8%; Score 2460; DB 2; Length 576;
Best Local Similarity 83.6%; Pred. No. 1.2e-176;
Matches 459; Conservative 44; Mismatches 38; Indels 8; Gaps 2;

```
Qy      1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
          ||||:|||||||||||||:|||:|||::|||:|||||||||||||:||:||||||||||
Db      1 MEFRKEEFKKLAGNTLGHLHRILEKKQKNGETIELTEEGQPVVKEEKHQPVVDCTCFGLP 60

Qy     61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
          |||||||||||||||||||||||||||||:|||:|:||||:|||:||::|||||||||||
Db     61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNNTVKGNKLVIEQAQFNWDPETVGMIH 120

Qy    121 GSFFWGYIVTQIPGGFICQKFAANRVPGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
          ||||||||||||||||||||||||||:|||||||||||||:|||||||:||:||||||||
Db    121 GSFFWGYIVTQIPGGYICQKFAANRVFGFAIVATSTLNMLIPSAARVHFACVICVRILQG 180

Qy    181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy    241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
          ||||||||:|||||||||||||:||||||:|:||:||||:|:||||||:||||||||||
Db    241 YGSFGIFWYMFWLLVSYESPAQHPTISEEERKYIEESIGESTGFMNDMAKFPAPWRKFFT 300

Qy    301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 SMPVYAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy    361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
          ||||:|:||||||||||||:|||||||||||||||||||||:|||||||||||||||||
Db    361 IADFLRTRRIMSTTNVRKVMMNCGGFGMEATLLLVVGYSHSRGVAISFLVLAVGFSGFAIS 420

Qy    421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy    481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
          ||||:||||||||||||||||||::|||||||||:|:||:|:|::|::---------||
Db    481 GGVVFYGIFASGEKQPWAEPEETSDEKCGFIHEDELA---DESEEQTQAH-----GGYGS 532

Qy    541 YGATHSTFQ 549
          ||||:|:|
Db    541 YGATHSTFQ 549
```

Db   533 YGATQTTSQ 541

RESULT 5

ID   Q715L3;   PRELIMINARY;   PRT;   576 AA.
AC   Q715L3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Glutamate transporter.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=12915319; DOI=10.1016/S1567-133X(03)00057-7;
RA   Gleason K.K., Dondetti V.R., Hsia H.L.J., Cochran E.R.,
RA   Gumulak-Smith J., Saha M.S.;
RT   "The vesicular glutamate transporter 1 (xVGlut1) is expressed in
RT   discrete regions of the developing Xenopus laevis nervous system.";
RL   Gene Expr. Patterns 3:503-507(2003).
DR   EMBL; AF548627; AAQ12345.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR007114; MFS.
DR   PROSITE; PS50850; MFS; 1.
SQ   SEQUENCE 576 AA; 63919 MW; 9262CA07FA4A49D1 CRC64;

Query Match   82.3%; Score 2444; DB 2; Length 576;
Best Local Similarity   84.0%; Pred. No. 2e-175;
Matches 461; Conservative 37; Mismatches 43; Indels 8; Gaps 2;

Qy   1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCPGLP 60
              |||||:| ||||||||||:|||::|||:::||||| ||| |||||||||||||||||||||
Db   1 MEFRKDEFKLAGNTLGRLHRILEKRQTNGETIELTEEGQPVVKEEKQPVVDCTCFGLP 60

Qy   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQPSWDPETVGLIH 120
              ||:||||||||||||||:|||||||||||||:||||||||||:..:||:||||||||||:|
Db   61 RRVIIAIMSGLGFCISFGIRCNLGVAIVSMVNNNTVYGISLLSSKRSSSWDPETVGMIH 120

Qy   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVAITSTLNMLIPSAARVHYGCVIFVRILQG 180
              |||:||||||||||||:||||||||:||||||||:||||||||||||||:|||||||||||
Db   121 GSFLWGYIVTQIPGGFICQKFAANRVFGFAIVAISTLLMLIPSAARVFPTCVIFVRILQG 180

Qy   181 LVEGVTYPACHGIWSKWAPPLERSRIATTAFCGSYAGAVVAMPLAGVLVQYSGWMSSVFYV 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
Db   181 LVEGVTYPACHGIWSKWAPPLERRELATTAFCGSYAGAVVAMPLAGVLVQYSGWSSSVFYV 240

Qy   241 YGSFGIMWYFWLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFPT 300
              |:||:||||||||:||||||||||||||||||||||||||||||||||||||||||||:|
Db   241 YGSFGLMWYMFWMLVSYESPAEHPSISEEERKYIEESIGESTGLMNPLTKFKAPWRKFFT 300

Qy   301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFGEISKVGLVSALPHLVMTIIVPIGGQ 360
              |||||||||||||||||||||||||||| |||||||||:|||:||||||||:|||||||||
Db   301 SMPVYAIIVANFCRSWTFYLLLISOPAYFEEVGFGEISKVGLISALPLHVMTIIVPIGGQ 360

Qy   361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVGYSHSKGVAISFLVLAVGFSGFAIS 420
              |||||||:|||||||||||||:|||||||||||||||||||||||||:||||||||||||
Db   361 IADFLRTRRIMSTTNVRKMMNCGGFGMEATLLLVGYSHSRGVAISFLVLAVGFSGFAIS 420

Qy   421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
              |||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db   421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPLIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
              ||||||||||:|||||||||||||||||||||||||||||||||||||||::||||||||
Db   481 GGVLFYGIFASGEKQPWABPEETSEEKCGFIHEDELA---DESEEQTQAF----GGYGS 532

Qy   541 YGATHSTFQ 549
              |||| :|:|
Db   533 YGATQTTSQ 541

Db   533 YGATQTTSQ 541

RESULT 6

ID   Q8AW47;   PRELIMINARY;   PRT;   584 AA.
AC   Q8AW47;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   SI:PACKT73.2 (Novel protein similar to human solute carrier family 17
DE   (Sodium-dependent inorganic phosphate cotransporter), member 6
DE   (SLC17A6)).
GN   Name=SI:PACKT73.2;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lloyd D.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL627170; CAD52142.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR007114; MFS.
DR   PROSITE; PS50850; MFS; 1.
SQ   SEQUENCE 584 AA; 64122 MW; 91C140D929E885DB CRC64;

Query Match   78.7%; Score 2338.5; DB 2; Length 584;
Best Local Similarity   80.3%; Pred. No. 1.7e-167;
Matches 436; Conservative 47; Mismatches 55; Indels 5; Gaps 2;

Qy   3 FRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCPGLPRR 62
              ||:|||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db   10 FSKEGLKQLAGKTLGHVVRVIEKRQKPGENIELTEDGRPAQINERKAPLCDCTCFGLPRR 69

Qy   63 YIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVV-QKAQFSWDPETVGLIHG 121
              ||||||||||||||||||||||||||||||||:|||||||:. :||.:||||||||||:|
Db   70 YIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTIHLNGKIIIKEKAKFNWDPETVGLIHG 129

Qy   122 SFFWGYIVTQIPGGFICQKFAANRVFGFAIVAITSTLNMLIPSAARVHYGCVIFVRILQGL 181
              |||||||||||||||||||||||||||||||||:|||||||||||||:||||||||||:||
Db   130 SFFWGYIVTQIPGGYISSRLAANRVFGAAILLTSTLNMFIPSAARGHYGCVIFVRILQGL 189

Qy   182 VEGVTYPACHGIWSKWAPPLERSRIATTAFCGSYAGAVVAMPLAGVLVQYSGWSSSVFYYX 241
              |||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||:.
Db   190 VEGVTYPACHGIWSKWAPPLERSRLATTSFCGSYAGAVVAMPLAGIILVQYTGWSSVFYYX 249

Qy   242 GSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTS 301
              ||||||||:||||||||||||||:||||:||||||||||||||||||||||||||||||||
Db   250 GCFGIFWYMFWILLVSYESPAEHPIITAERCYIEESIGESAKLLGPADKFKTPWRKFFTS 309

Qy   302 MPVYAIIVANFCRSWTFYLLLISQPDYEEVGFGEISKVGLVSALPHLVMTIIVPIGGQI 361
              ||||||||||||||||||||||| ||::|||||||||||:||||||||||||||||||||
Db   310 MPVYAIIVANFCRSWTFYLLLISQPAYFEEVGFGEISKVGMLSALPHLVMTIIVPIGGQL 369

Qy   362 ADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVGYSHSKGVAISFLVLAVGFSGFAISG 421
              ||||||||||||||||||||:||||||||||||||||||||||||||:||||||||||||
Db   370 ADHLRSKNILSTTTVRKIMNCGGFGMEATLLLVGYSHSKGVAISFLVLAVGFSGFAISG 429

Qy   422 FNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYG 481
              ||||||||||||||:|||||||||||||||||||||||||||||||||:||||||||||||
Db   430 FNVNHLDIAPRYASILMGISNGVGTLSGMVCPLIVGAMTKHKTREEWQYVFLIASLVHYG 489

Qy   482 GVIFYGVFASGEKQPWABPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPSY 541
              ||:||||:||||||||||||||:|||||||||||||||||||||||||:::||||||| |
Db   490 GVIFYGIFASGEKQPWADPELTSDEKCGFIDEDELA----EETGDITQSYGALGAPAKSY 545

Qy   542 GAT 544
              |||
Db   542 GAT 544

RESULT 7

Db   Q9P2U8
      |||
      546 GAT 548

ID   Q9P2U8   PRELIMINARY;   PRT;   582 AA.
AC   Q9P2U8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Differentiation-associated Na-dependent inorganic phosphate
DE   cotransporter (Differentiation-associated Na-dependent inorganic
DE   phosphate cotr).
GN   Name=DNPI; Synonyms=SLC17A6;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain thalamus;
RX   MEDLINE=20281869; PubMed=10820226;
RA   Aihara Y., Mashima H., Onda H., Hisano S., Kasuya H., Hori T.,
RA   Yamada S., Tomura H., Yamada Y., Inoue I., Kojima I., Takeda J.;
RT   "Molecular cloning of a novel brain-type Na(+)-dependent inorganic
RT   phosphate cotransporter.";
RL   J. Neurochem. 74:2622-2625(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PCR rescued clones;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PCR rescued clones;
RP   Director MGC Project;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB032435; BAA92874.1; -.
DR   EMBL; BC069629; AAH69629.1; -.
DR   EMBL; BC069640; AAH69640.1; -.
DR   EMBL; BC069646; AAH69646.1; -.
DR   Genew; HGNC:16703; SLC17A6.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR007114; MFS.
DR   PROSITE; PS50850; MFS; 1.
SQ   SEQUENCE   582 AA;   64392 MW;   CE761E56FA18C6AD CRC64;

Query Match   78.0%;   Score 2317.5;   DB 2;   Length 582;
Best Local Similarity   79.4%;   Pred. No. 6.6e-166;
Matches 429;   Conservative 56;   Mismatches 50;   Indels 5;   Gaps 2;

Qy   5 QEEFPRKLAGRGRALGGKLHRILLEKRQEGAETLELSLADGRPVTTQTRDPPVVDCTCFGLPRRYI 64
        : ||||| ||| |||:| :|||:|||| : |:||:|:: |: ||:|: ||| |||||||||
Db   13 KEGLIKNFAGKSLGQIYRVLEKKQDTGETIELIEDGKPLEVPERKAPLCDCTCFGLPRRYI 72

Qy   65 IAIMSGLGFCISPGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFF 124
        |||||||||||||||||||||||||:||||||:|:: |::|:|:||| |:|||||||||||
Db   73 IAIMSGLGFCISPGIRCNLGVAIVDMVNNSTIHRGGKVIKEAKFNWDPETVGMIHGSFF 132

Qy 125 WGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEG 184
        |||||||||||| :||||||||||||:||:|:||||:|||||||| :|:|||||||| |
Db 133 WGYIITQTPGGYIASRLAANRVFGAAILLTSTLNMLIPSAARVHYGCVIFVRILQGLVEG 192

Qy 185 VTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYVVGSF 244
        |||||| ||||||||||||||||:|||||||||| |||||| ||||||:||:|:|||||||
Db 193 VTYPACHGIWSKWAPPLERSRLATTSFCGSYAGAVIAMPLAGVLVQYTGWSSVFYVVGSF 252

Qy 245 GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLITKFSTPWRRFFTSMPV 304
        ||:|||||||||| ||||||:|:|||||||||:||::| ||||:||: |||| |||||||
Db 253 GMVWYMFWLLVSYESPAKHPTITDEERRYIEBSIGESANLLGAMEKFKTPWRRFFTSMPV 312

Qy 305 YAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADF 364
        ||||||| ||||||||||:||:| |::||||||||||||||:|:|::||||:||||||||
Db 313 YAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGMLSAVPHLVMTIIVPIGGQIADF 372

Qy 365 LRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGENV 424
        |||||||||||||||| ||||||||:||||||||:|:||:|:||||||||||||||||||
Db 373 LRSKQILSTTTVRKIMNCGGFGMEATLLLVVGYSHTRGVAISFLVLAVGFSGFAISGFNV 432

Qy 425 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVI 484
        ||||||||||||||||||||||||||||||||||||||| :|:|||:||:||:||||||||
Db 433 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKNKSREEWQYVFLIAALVHYGGVI 492

Qy 485 FYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPAPPSYGAT 544
        |||||:|||||||| :||| ||||| ||||||:| |: || :| || ||||||
Db 493 FYAIFASGEKQPWADPEETSEBKCGFIHEDEL----DEETGDITQ-NYINGGTTKSYGAT 547

RESULT 8

ID   Q920B7   PRELIMINARY;   PRT;   582 AA.
AC   Q920B7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Vesicular glutamate transporter 2 (Solute carrier family 17 (Sodium-
DE   dependent inorganic phosphate cotransporter), member 6).
GN   Name=Slc17a6;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21453279; PubMed=11432869; DOI=10.1074/jbc.M104578200;
RA   Bai L., Xu H., Collins J.F., Ghishan F.K.;
RT   "Molecular and functional analysis of a novel neuronal vesicular
RT   glutamate transporter.";
RL   J. Biol. Chem. 276:36764-36769(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RESULT 9

RA   Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF324864; AAL08941.1; -.
DR   EMBL; BC038375; AAH38375.1; -.
DR   MGD; MGI:2156052; Slc17a6.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0008021; C:synaptic vesicle; IDA.
DR   GO; GO:0005313; F:L-glutamate transporter activity; IDA.
DR   GO; GO:0005504; P:neurotransmitter uptake; IDA.
DR   PROSITE; PS50850; MFS; 1.
SQ   SEQUENCE   582 AA; 64559 MW; 9F7A4F62E685A8AD CRC64;

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Query Match   Best Local Similarity   77.9%;
                            Conservative   79.3%;   Score 2313.5;   DB 2;   Length 582;
Matches  428;   Conservative  57;   Pred. No. 1.3e-165;   Indels  5;   Gaps  2;

Qy    5 QEEFRKLAGRALGKLHRLLEKRQEGAETELELSADGRPVTQTRDDPPVVDCTCFGLPRRYI   64
          ||:|||||||| ||:|||:|||:|.|:.||||:   :|.: | ||:|:|:||||||
Db   13 KEGIKNFAGKSLGQIYRVLEKKQDNREITELTEDEGKPLEVPEKKAPLCDCTCFGLPRRYI   72

Qy   65 IAIMSGLGPCISFGIRCNLGVAIVSMVNNSTIHRGGHVVVQKAQFSWDPETVGLIHGSFF  124
         ||||||||||||||||||||||| ||||||||||| :|   |...|| |::|.|:||||
Db   73 IAIMSGLGPCISFGIRCNLGVAIVDMVNNSTIHRGGKVIKEKAKFNWDPETVGMIHGSFF  132

Qy  125 WGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEG  184
         |||| |||||| |  |:||||||| || |||||||||||||||||||||||||||||||
Db  133 WGYIITQIPGGYIASRLAANRVFGAAILLTSTLNMLIPSAARVHYGCVIFVRILQGLVEG  192

Qy  185 VTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYVYGSF  244
         ||||||||||||||||||||||||:||||||||:|||||||:|||| |||||:|:||||
Db  193 VTYPACHGIWSKWAPPLERSRLATTSFCGSYAGAVIAMPLAGIIVQYTGWSSVFYVYGSF  252

Qy  245 GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPV  304
         | :|::||||||||||| ||:|:|||:||||:|||||:|:  |::|| |||::|||||||
Db  253 GMWYMFWLLVSYESPAKHPTITDEERRYIEESIGESANLLGAMEKFKIPWRKFFTSMPV  312

Qy  305 YAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQIADF  364
         |||||||||||||||||:|||| |||||||:|||||:||:|||||||||||||||||||
Db  313 YAIIVANFCRSWTFYLLIISQPAYFEEVGFGEISKVGMLSAVPHLVMTIIVPIGGQIADF  372

Qy  365 LRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFIVLAVGFSGFAISGFNV  424
         |||::|:||| |||:|||||||||||||||||||||::||||||:||||||||||||||||
Db  373 LRSKQILSTTTVRKIMNCCGFGMEATLLLVVGYSHTRGVAISFLVLAVGFSGFAISGFNV  432

Qy  425 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVI  484
         ||||||||||||||||||||||||||||||||||||::|:||||||||  :|||||||||
Db  433 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKNKSREEWQYVFLAALVHYGGVI  492

Qy  485 FYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPSYGAT  544
         || :||||||||| |||:|||||||:  |: |           :|||  | ||||||||
Db  493 FYALFASGEKQPWADPEETSEEKCGFIHEDEL---DEETGDITQ-NYINYGTTKSYGAT  547
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ID   Q9JI12   PRELIMINARY;   PRT;   582 AA.
AC   Q9JI12;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Differentation-associated Na-dependent inorganic phosphate
DE   cotransporter.
GN   Name=DNP1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Mashima H., Kojima I.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF271235; AAF76223.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR007114; MFS.
DR   PROSITE; PS50850; MFS; 1.
SQ   SEQUENCE   582 AA; 64575 MW; 99A14F62E685B9E9 CRC64;

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Query Match   Best Local Similarity   77.9%;
                            Conservative   79.3%;   Score 2313.5;   DB 2;   Length 582;
Matches  428;   Conservative  57;   Pred. No. 1.3e-165;   Indels  5;   Gaps  2;
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RESULT 10

Q8BLE7
ID   Q8BLE7   PRELIMINARY;   PRT;   582 AA.
AC   Q8BLE7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length
DE   enriched library, clone:B230114L05 product:solute carrier family 6,
DE   (sodium-dependent inorganic phosphate cotransporter), member 6, full
DE   insert sequence.
GN   Name=Slc17a6;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX   MEDLINE=99279253; PubMed=10349536; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   The RIKEN Genome Exploration Research Group Phase II Team;
RG   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX   MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX   MEDLINE=2053091; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto K., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RG   The FANTOM Consortium;
RG   RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka I., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   MGD; MGI:2156052; Slc17a6.
DR   EMBL; AK045409; BAC32349.1; -.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0008021; C:synaptic vesicle; IDA.
DR   GO; GO:0005313; F:L-glutamate transporter activity; IDA.
DR   GO; GO:0001504; P:neurotransmitter uptake; IDA.
DR   InterPro; IPR007114; MFS.
DR   PROSITE; PS50850; MFS; 1.
SQ   SEQUENCE 582 AA; 64560 MW; 9F7A47C0E0C7A64D CRC64;

Query Match             77.7%;  Score 2308.5;  DB 2;  Length 582;
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Best Local Similarity   79.1%;  Pred. No. 3.2e-165;
Matches   427;  Conservative  58;  Mismatches  50;  Indels   5;  Gaps   2;

Qy    5 QEEFRKLAGRALGKLHRLLEKRQEEGAETLELSADGRPVTTQTRDPPVVDCTCFGLPRRYI 64
          :||:|||:|| |:||:|||::|  |||:|:|::  |:|           |||||||||||
Db   13 KEGIKNFAGKSLGQIYRVLEKKQQDNRETIELTEDGKPLEVPEKKAPLCDCTCFGLPRRYI 72

Qy   65 IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFF 124
         ||||||||||||||||||||||||.|||||| ||||:|: : |: :|||||||:|||||
Db   73 IAIMSGLGFCISFGIRCNLGVAIVDMVNNSTIHRGGKVIKEAKFNWDPETVGMIHGSFF 132

Qy  125 WGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEG 184
         ||||:||||| | ::::AANRVFG AI: :TSTLNMLIPSAARVHYGCVIFVRILQGLVEG
Db  133 WGYIITQIPGGYIASRLAANRVFGAAILLTSTLNMLIPSAARVHYGCVIFVRILQGLVEG 192

Qy  185 VTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVPYVYGSF 244
         |||||||| ||||||||||||||||:|||||||||:|||||| :|||:|||||||||||
Db  193 VTYPACHGTWSKWAPPLERSRLATTSFCGSYAGAVIAMPLAGIIVQYTGWSSVPYVYGSF 252

Qy  245 GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPV 304
         | :|: :||||||||||:||:::::||:|||:|||||| :: : ::||:|||:|||||||
Db  253 GMWYMYFWLLVSYESPAKHPITTDEERRYIEESIGESANILGAMEKFKPWRKFFTSMPV 312

Qy  305 YAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADF 364
         |||||||||||||||||:|||| ||||||||||||||::||:||||||||||||||||||
Db  313 YAIIVANFCRSWTFYLLIISQPAYFEEVFGFEISKVGMLSAVPHLVMTIIVPIGGQIADF 372

Qy  365 LRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGFNV 424
         |||::|:STT VRK:MNCGGFGMEATLLLVVGYSH::GVAISFLVLAVGFSGFAISGFNV
Db  373 LRSKQILSTTTVRKIMNCGGFGMEATLLLVVGYSHTRGVAISFLVLAVGFSGFAISGFNV 432

Qy  425 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIIASLVHYGGVI 484
         |||||||||||||||||:|||||||||||||||||:::|:REEWQYVFLI:A LVHYGGVI
Db  433 NHLDIAPRYASILMGISDGVGTLSGMVCPIIVGAMTQNKSREEWQYVFLIAALVHYGGVI 492

Qy  485 FYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDRAEPPGGAPPAPPPSYGAT 544
         ||.:|||||||||::|||.|||||||:|::||          :::::  |      ||||
Db  493 FYALFASGEKQPWADPEETSEEKCGFIHEDEL----DEETGDITQ-NYINYGTTKSYGAT 547
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RESULT 11
Q8K1Q1
ID   Q8K1Q1      PRELIMINARY;      PRT;    588 AA.
AC   Q8K1Q1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Vesicular glutamate transporter 3.
GN   Name=vglut3;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague Dawley; TISSUE=Brain;
RX   MEDLINE=22092356; PubMed=12097496;
RA   Gras C., Herzog E., Bellenchi G.C., Bernard V., Ravassard P., Pohl M.,
RA   Gasnier B., Giros B., El Mestikawy S.;
RT   "A third vesicular glutamate transporter expressed by cholinergic and
RT   serotoninergic neurons.";
RL   J. Neurosci. 22:5442-5451(2002).
DR   EMBL; AJ491795; CAD37138.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR007114; MFS.
DR   PROSITE; PS00290; IG_MHC.
DR   PROSITE; PS50850; MFS; 1.
SQ   SEQUENCE 588 AA; 64754 MW; 9644C021D9428EB5 CRC64;

Query Match             74.0%;  Score 2198;  DB 2;  Length 588;
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RESULT 12

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Best Local Similarity   76.9%;  Pred. No. 6.7e-157;
Matches  415;  Conservative  50;  Mismatches  69;  Indels  6;  Gaps  3;

Qy      5 QEEFRKLAGRALGKIHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLPRRYI   64
            :|||||||||||||||||||||||||||:||||||:|||||||||||||||||| ||||||
Db      5 QEEFRKLAGRALGKIHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLPRRYI   64

Qy     18 KEGVKNAVGDSLGILQRKLDGTNEEGDAIELSEEGRPVQTSRARAPVCDCSCCGIPKRYI   77
            |||||||||||||||||||||||||||||||||||||| ||||||||||:||||||||||
Db     18 KEGVKNAVGDSLGILQRKLDGTNEEGDAIELSEEGRPVQTSRARAPVCDCSCCGIPKRYI   77

Qy     65 IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFF  124
            |:||||||||||||||||||||||||||||||||||||||:|||||||:|||||||||||
Db     65 IAIMSGLGFCISFGIRCNLGVAIVEMVNNSTVVVDGKPEIQTAQFNWDPETVGLIHGSFF  124

Qy     78 IAVMSGGGFCISFGIRCNLGVAIVEMVNNSTVVVDGKPEIQTAQFNWDPETVGLIHGSFF  137
            |:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     78 IAVMSGGGFCISFGIRCNLGVAIVEMVNNSTVVVDGKPEIQTAQFNWDPETVGLIHGSFF  137

Qy    125 WGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEG  184
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    138 WGYIVTQIPGGFISNKFAANRVFGAAIFLTSTLNMFIPSAARVHYGCVMCVRILQGLVEG  197

Qy    138 WGYIVTQIPGGFISNKFAANRVFGAAIFLTSTLNMFIPSAARVHYGCVMCVRILQGLVEG  197
            ||||||||||||:::||||||||:|||:|||||||:|||||||||||:|:||||||||||
Db    185 VTYPACHGIWSKWAPPLERSRLATTAFCCGSYAGAVVAMPLAGVLVQYSGWSSSVFYVYGSF  244

Qy    185 VTYPACHGIWSKWAPPLERSRLATTAFCCGSYAGAVVAMPLAGVLVQYSGWSSSVFYVYGSF  244
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    198 VTYPACHGMWSKWAPPLERSRLATTSFCCGSYAGAVVAMPLAGVLVQYIGWASVFYIYGMF  257

Qy    198 VTYPACHGMWSKWAPPLERSRLATTSFCCGSYAGAVVAMPLAGVLVQYIGWASVFYIYGMF  257
            ||||||||||||:::|||||||||||||||||||||:||||||||:|::|||||:||
Db    245 GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPV  304

Qy    245 GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPV  304
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    258 GIIWYMFWLLQAYECPAVHPTISNEERTYIETSIGEGANLAS-LSKFNTPWRRFFTSLPV  316

Qy    258 GIIWYMFWLLQAYECPAVHPTISNEERTYIETSIGEGANLAS-LSKFNTPWRRFFTSLPV  316
            ||||||||||||:|::|||||:||||||:|||:|||||||||||:||||||||||||||
Db    305 YAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLIVSALPHLVMTIIVPIGGQIADF  364

Qy    305 YAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLIVSALPHLVMTIIVPIGGQIADF  364
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    317 YAIIVANFCRSWTFYLLLISQPAYFEEVFGFAISKVGLLSAVPHMVMTIVVPIGGQLADY  376

Qy    317 YAIIVANFCRSWTFYLLLISQPAYFEEVFGFAISKVGLLSAVPHMVMTIVVPIGGQLADY  376
            ||||||||||||||||||||||:|||||||||:||||||:||||:||||:||||||||:
Db    365 LRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGFNV  424

Qy    365 LRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGFNV  424
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    377 LRSRKILTITAVRKIMNCCGFGMEATLLLVVGFSHTKGVAISFLVLAVGFSGFAISGFNV  436

Qy    377 LRSRKILTITAVRKIMNCCGFGMEATLLLVVGFSHTKGVAISFLVLAVGFSGFAISGFNV  436
            ||||:||||:||||||||:||||||||||||:||:|||||||||||||||||||||||
Db    425 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVI  484

Qy    425 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVI  484
            ||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db    437 NHLDIAPRYASILMGISNGVGTLSGMVCPLIVGAMTKHKTREEWQNVFLIAALVHYSGVI  496

Qy    437 NHLDIAPRYASILMGISNGVGTLSGMVCPLIVGAMTKHKTREEWQNVFLIAALVHYSGVI  496
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    485 FYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPSYGAT  544

Qy    485 FYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPSYGAT  544
            |||||||||||:|||||||||||||||||||||||||||       |::|||||||||
Db    497 FYGVFASGEKQDWADPENLSEEKCGIIDQDELA--EETELNHEA---FVSPRKMSYGAT  551

Qy    497 FYGVFASGEKQDWADPENLSEEKCGIIDQDELA--EETELNHEA---FVSPRKMSYGAT  551
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ID   Q7TSF2
AC   Q7TSF2;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Vesicular glutamate transporter 3.
GN   Name=Vglut3;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Liver;
RA   Fremeau R.T. Jr., Burman J.L., Qureshi T., Tran C.H., Proctor J.,
RA   Johnson J., Zhang H., Sulzer D., Copenhagen D.R., Storm-Mathisen J.,
RA   Reimer R.J., Chaudhry F.A., Edwards R.H.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY117026; AAM50094.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR003006; IG_MHC.
DR   InterPro; IPR007114; MFS.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR   PROSITE; PS50850; MFS; 1.
SQ   SEQUENCE 588 AA; 64768 MW; 97B1A5801D272684 CRC64;

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Query Match        74.0%;  Score 2198;  DB 2;  Length 588;
Best Local Similarity  76.9%;  Pred. No. 6.7e-157;
Matches  415;  Conservative  50;  Mismatches  69;  Indels  6;  Gaps  3;
```

RESULT 13

```
Best Local Similarity   76.9%;  Pred. No. 6.7e-157;
Matches  415;  Conservative  50;  Mismatches  69;  Indels  6;  Gaps  3;

Qy      5 QEEFRKLAGRALGKIHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLPRRYI   64
Db      5 QEEFRKLAGRALGKIHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLPRRYI   64

Qy     18 KEGVKNAVGDSLGILQRKLDGTNEEGDAIELSEEGRPVQTSRARAPVCDCSCCGIPKRYI   77
Db     18 KEGVKNAVGDSLGILQRKLDGTNEEGDAIELSEEGRPVQTSRARAPVCDCSCCGIPKRYI   77

Qy     65 IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFF  124
Db     65 IAIMSGLGFCISFGIRCNLGVAIVEMVNNSTVVVDGKPEIQTAQFNWDPETVGLIHGSFF  124

Qy     78 IAVMSGGGFCISFGIRCNLGVAIVEMVNNSTVVVDGKPEIQTAQFNWDPETVGLIHGSFF  137
Db     78 IAVMSGGGFCISFGIRCNLGVAIVEMVNNSTVVVDGKPEIQTAQFNWDPETVGLIHGSFF  137

Qy    125 WGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEG  184
Db    138 WGYIVTQIPGGFISNKFAANRVFGAAIFLTSTLNMFIPSAARVHYGCVMCVRILQGLVEG  197

Qy    138 WGYIVTQIPGGFISNKFAANRVFGAAIFLTSTLNMFIPSAARVHYGCVMCVRILQGLVEG  197
Db    185 VTYPACHGIWSKWAPPLERSRLATTAFCCGSYAGAVVAMPLAGVLVQYSGWSSSVFYVYGSF  244

Qy    185 VTYPACHGIWSKWAPPLERSRLATTAFCCGSYAGAVVAMPLAGVLVQYSGWSSSVFYVYGSF  244
Db    198 VTYPACHGMWSKWAPPLERSRLATTSFCCGSYAGAVVAMPLAGVLVQYIGWASVFYIYGMF  257

Qy    198 VTYPACHGMWSKWAPPLERSRLATTSFCCGSYAGAVVAMPLAGVLVQYIGWASVFYIYGMF  257
Db    245 GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPV  304

Qy    245 GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPV  304
Db    258 GIIWYMFWLLQAYECPAVHPTISNEERTYIETSIGEGANLAS-LSKFNTPWRRFFTSLPV  316

Qy    258 GIIWYMFWLLQAYECPAVHPTISNEERTYIETSIGEGANLAS-LSKFNTPWRRFFTSLPV  316
Db    305 YAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLIVSALPHLVMTIIVPIGGQIADF  364

Qy    305 YAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLIVSALPHLVMTIIVPIGGQIADF  364
Db    317 YAIIVANFCRSWTFYLLLISQPAYFEEVFGFAISKVGLLSAVPHMVMTIVVPIGGQLADY  376

Qy    317 YAIIVANFCRSWTFYLLLISQPAYFEEVFGFAISKVGLLSAVPHMVMTIVVPIGGQLADY  376
Db    365 LRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGFNV  424

Qy    365 LRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGFNV  424
Db    377 LRSRKILTITAVRKIMNCCGFGMEATLLLVVGFSHTKGVAISFLVLAVGFSGFAISGFNV  436

Qy    377 LRSRKILTITAVRKIMNCCGFGMEATLLLVVGFSHTKGVAISFLVLAVGFSGFAISGFNV  436
Db    425 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVI  484

Qy    425 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVI  484
Db    437 NHLDIAPRYASILMGISNGVGTLSGMVCPLIVGAMTKHKTREEWQNVFLIAALVHYSGVI  496

Qy    437 NHLDIAPRYASILMGISNGVGTLSGMVCPLIVGAMTKHKTREEWQNVFLIAALVHYSGVI  496
Db    485 FYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPSYGAT  544

Qy    485 FYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPSYGAT  544
Db    497 FYGVFASGEKQDWADPENLSEEKCGIIDQDELA--EETELNHEA---FVSPRKMSYGAT  551

Qy    497 FYGVFASGEKQDWADPENLSEEKCGIIDQDELA--EETELNHEA---FVSPRKMSYGAT  551
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ID   Q8NDX2
AC   Q8NDX2;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Vesicular glutamate transporter 3.
GN   Name=VGLUT3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22146126; PubMed=12151341; DOI=10.1093/embo-reports/kvf159;
RA   Takamori S., Malherbe P., Broger C., Jahn R.;
RT   "Molecular cloning and functional characterization of human vesicular
RT   glutamate transporter 3.";
RL   EMBO Rep. 3:798-803(2002).
DR   EMBL; AJ459241; CAD30553.1; -.
DR   Genew; HGNC:20151; SLC17A8.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR003006; IG_MHC.
DR   InterPro; IPR007114; MFS.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR   PROSITE; PS50850; MFS; 1.
SQ   SEQUENCE 589 AA; 64991 MW; E74DDC91495F8775 CRC64;

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Query Match        73.6%;  Score 2185;  DB 2;  Length 589;
Best Local Similarity  76.3%;  Pred. No. 6.4e-156;
Matches  412;  Conservative  53;  Mismatches  69;  Indels  6;  Gaps  3;
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Qy    5  QEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLPRRYI   64
         ||||||||||||||||||||:||: :
Db   18  KEGVKNAVGDSLGILQRKIDGTTEEEDNIEIELNEEGRPVQTSRPSPPLCDCHCCGLPKRYI   77

Qy   65  IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFF  124
         ||||||||||||||||||||||| |||| ||
Db   78  IAIMSGLGFCISFGIRCNLGVAIVEMVNNNSTVVYDGKPEIQTAQFNWDPETVGLIHGSFF  137

Qy  125  WGYIVTQIPGGFICQKFPAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEG  184
         |||||  |||||| |:||||||||:||::|||||||:||||||||||||: |||||||||
Db  138  WGYIVMFQIPGGFISNKFAANRVFGAAIFLTSTLNMFIPSAARVHYGCVMCVRILQGLVEG  197

Qy  185  VTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYVYGSF  244
         ||||||| |||||||||||||||||:||||||||||||||||||||| |||||||:||:|
Db  198  VTYPACHGMWSKWAPPLERSRLATTSFCGSYAGAVVAMPLAGVLVQYIGWSSVFYIYGMF  257

Qy  245  GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPV  304
         || ||:|||| :|| |||||:|::||:||||:|||:||:::||||||||||:|||||:||
Db  258  GIWWYMFWLLQAYECPAAHPTISNEEKTYIETSIGEGANVVS-LSKFSTPWKRFFTSLPV  316

Qy  305  YAIIVANFCRSWTFYLLLISQPDYEEVFGFEISKVGLVSALPHLVMTIIVPIGGIADF  364
         ||||||||||||||||||||||  :|||||:||||||:|||||:||||||||||| ||:
Db  317  YAIIVANFCRSWTFYLLLISQPAYFEEVFGFAISKVGLLSAVPHMVMTIIVPIGGQLADY  376

Qy  365  LRSRSRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGFNV  424
         ||||  : ||:|||:||||||||||||||||||:|:|||||||||||||||||||||||||
Db  377  LRSRQILTTAVRKIMNCGGFGMEATLLLVVGFSHTKGVAISFLVLAVGFSGFAISGFNV  436

Qy  425  NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTHGHKTREEWQYVFLIASLVHYCGVI  484
         |||||||||||||||||||||||||||||:||||||  |||||||| ||||:|||||:|||
Db  437  NHLDIAPRYASILMGISNGVGTLSGMVCPLIVGAMTRHKTREEWQNVFLIAALVHYSGVI  496

Qy  485  FYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPSYGAT  544
         |||||||||| ||:|| :||:||||: :|||: | :: ||:|  | :  |  :||||||
Db  497  FYGVFASGEKQEWADPENLSEDKCGIIDQDELA--EEIELNHES---FASPKKKMSYGAT  551
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RESULT 14
Q8BFU8
ID   Q8BFU8        PRELIMINARY;       PRT;   601 AA.
AC   Q8BFU8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Vesicular glutamate transporter-3.
GN   Name=Slc17a8; Synonyms=Vglut3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RG   Director MGC Project;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Whole brain;
RX   PubMed=12384506; DOI=10.1074/jbc.M206738200;
RA   Schafer M.K., Varoqui H., Defamie N., Weihe E., Erickson J.D.;
RT   "Molecular cloning and functional identification of mouse vesicular
RT   glutamate transporter 3 and its expression in subsets of novel
RT   excitatory neurons.";
RL   J. Biol. Chem. 277:50734-50748(2002).
DR   EMBL; BC042593; AAH42593.1; -.
DR   EMBL; AF510321; AAN74643.1; -.
DR   MGD; MGI:3039629; Slc17a8.
DR   GO; GO:0030672; C:synaptic vesicle membrane; IDA.
DR   GO; GO:0005313; F:L-glutamate transporter activity; IDA.
DR   GO; GO:0015813; P:L-glutamate transport; IDA.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR007114; MFS.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR   PROSITE; PS00850; MFS; 1.
SQ   SEQUENCE   601 AA;  66148 MW;  EBF6FC6E0C64961B CRC64;

Query Match             72.5%;  Score 2154.5;  DB 2;  Length 601;
Best Local Similarity   74.0%;
Matches  409;  Conservative  53;  Mismatches  72;  Indels  19;  Gaps  4;
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Qy    5  QEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPV------------   51
         :  |  :||  : |::  || |:::   |  :  ||   :: |  ::
Db   18  KEGVKNAVGDSLGILQRKIDGTNEEEDAIEIELNEEGRPVCDCSCCGIPKRYI         77

Qy   52  VDCTCFGLPRRYIIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSW  111
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   78  CDCSCCGIPKRYIIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSW  137

Qy  112  DPETVGLIHGSFFWGYIVTQIPGGFICQKFPAANRVFGFAIVATSTLNMLIPSAARVHYGC  171
         |||||||||||||||||||  ||||| |:||||||||:||||||||||||:||||||||||
Db  138  DPETVGLIHGSFFWGYIVTQIPGGFISNKFAANRVFGAAIFLTSTLNMFIPSAARVHYGC  197

Qy  172  VIFVRILQGLVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQY  231
         |: |||||||||||||||| ||||||||||||||||||:|||||||||||||||||||||
Db  198  VMCVRILQGLVEGVTYPACHGMWSKWAPPLERSRLATTSFCGSYAGAVVAMPLAGVLVQY  257

Qy  232  SGWSSVFYVYGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKF  291
          |||||||:||:||| ||:|||| :|| |||||:|::||:||||:|||:||:::|||||
Db  258  IGWSSVFYIYGMFGIWWYMFWLLQAYECPAAHPTISNEEKTYIETSIGEGANVVS-LSKF  316

Qy  292  STPWRRFFTSMPVYAIIVANFCRSWTFYLLLISQPDYEEVFGFEISKVGLVSALPHLVM  351
         |||||:|||||::|||||||||||||||||||||||  :|||||:||||||:||||||:|
Db  317  STPWKRFFTSLPVYAIIVANFCRSWTFYLLLISQPAYFEEVFGFAISKVGLLSAVPHMVM  376

Qy  352  TIIVPIGGIADFLRSRSRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLA  411
         |||||||||| |:||||  : ||:|||:||||||||||||||||||:|:||||||||||||
Db  377  TIIVPIGGQLADYLRSRQILTTAVRKIMNCGGFGMEATLLLVVGFSHTKGVAISFLVLA  436

Qy  412  VGFSGFAISGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTHGHKTREEWQYV  471
         |||||||||||||||||||||||||||||||||||||||||||:||||||  ||||||||
Db  437  VGFSGFAISGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPLIVGAMTRHKTREEWQNV  496

Qy  472  FLIASLVHYCGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPP  531
         ||||:|||||:|||||||||||| ||:|| :||:||||: :|||: | :: ||:|  |
Db  497  FLIAALVHYSGVIFYGVFASGEKQEWADPENLSEDKCGIIDQDELA--EEIELNHET--  551

Qy  532  GAPPAPPPSYGAT  544
              | :||||||
Db  552  FVSPRKKMSYGAT  564
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RESULT 15
Q7TQH3
ID   Q7TQH3      PRELIMINARY;     PRT;    402 AA.
AC   Q7TQH3;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Solute carrier family 17 (Sodium-dependent inorganic phosphate
DE   cotransporter), member 7.
GN   Name=Slc17a7;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RA   Director MGC Project;
RT   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
RL   EMBL; BC054462; AAH54462.1; -.
DR   GO; GO:0042137; P:neurotransmitter storage; IMP.
DR   InterPro; IPR007114; MFS.
DR   PROSITE; PS50850; MFS; 1.
SQ   SEQUENCE   402 AA;  44140 MW;  62844306CB033DD0 CRC64;

Query Match             70.9%;
Best Local Similarity   98.5%;
Matches  396;  Conservative   3;  Mismatches   3;  Indels   0;  Gaps   0;

Qy    159 MLIPSAARVHYGCVIFVRILQGLVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGA 218
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db      1 MLIPSAARVHYGCVIFVRILQGLVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGA 60

Qy    219 VVAMPLAGVLVQYSGWSSVFYYVGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAI 278
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 VVAMPLAGVLVQYSGWSSVFYYVGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAI 120

Qy    279 GESAKLMNPLTKFSTPWRRFFTSMPVAIIVANFCRSWTFYLLLISQDYFEEVFGFEIS 338
          ||||||| :|||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GESAKLMNPVTKPNTPWRRFFTSMPVAIIVANFCRSWTFYLLLISQAYFEEVFGFEIS 180

Qy    339 KVGLVSALPHLVWTIIVPIGGQIADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYS 398
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 KVGLVSALPHLVWTIIVPIGGQIADFLRSRHIMSTTNVRKLMNCGGFGMEATLLLVVGYS 240

Qy    399 HSKGVAISFLVLAVGFSGGFAIGGFNVANHLDIAPRYASILMGISNGVGTLSGMVCPIIVGA 458
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 HSKGVAISFLVLAVGFSGGFAIGGFNVANHLDIAPRYASILMGISNGVGTLSGMVCPIIVGA 300

Qy    459 MTKHKTREEWQYVFLIASLVHYGGVIFYGVPASGEKQPWAEPEEMSEEKCGFVGHDQLAG 518
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MTKHKTREEWQYVFLIASLVHYGGVIFYGVPASGEKQPWAEPEEMSEEKCGFVGHDQLAG 360

Qy    519 SDDSEMEDEAEPPGAPPAPPPSYGATHSTFQPPRPPPVRDY 560
          ||:||||||||||||||||||||||||||||| |||||||||
Db    361 SDESEMEDEAEPPGAPPAPPPSYGATHSTVQPPRPRPPVRDY 402

                    Score 2107;  DB 2;  Length 402;
                    Pred. No. 3e-150;
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OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: June 2, 2005, 11:17:01 ; Search time 163 Seconds
(without alignments)
1328.747 Million cell updates/sec

Title: US-10-734-731-4
Perfect score: 2970
Sequence: 1 MEFRQEEFRKLAGRALGKLH..........YGATHSTFQPRPRPPPVPRDY 560

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_16Dec04:*
                1: geneseqp1980s:*
                2: geneseqp1990s:*
                3: geneseqp2000s:*
                4: geneseqp2001s:*
                5: geneseqp2002s:*
                6: geneseqp2003as:*
                7: geneseqp2003bs:*
                8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%	Query Match Length	DB	ID	Description
1	2970	100.0	560	2	Aaw05148	Human bra
2	2970	100.0	560	6	Abg74792	Human BNP
3	2970	100.0	560	6	Adc15484	Human BNR
4	2967	99.9	560	2	Aaw70500	Human sod
5	2962	99.7	560	7	Abg74791	Human BNP
6	2962	99.7	560	6	Adc15482	Human BNP
7	2962	99.7	560	7	Add01474	Human VGL
8	2962	99.7	567	4	Aao13870	Human pol
9	2929	98.6	567	6	Abg74794	Murine BN
10	2929	98.6	560	7	Abg74794	Murine BN
11	2925	98.5	560	6	Abg74793	Rat BNPI
12	2925	98.5	560	6	Adc15486	Rat BNPI
13	2317.5	78.0	582	6	Abg74795	Human BNP
14	2317.5	78.0	582	6	Adc15490	Human DNP
15	2317.5	78.0	582	7	Add01475	Human VGL
16	2313.5	77.9	578	7	Adg88331	Rat trans
17	2313.5	77.9	582	6	Abg74796	Rat DNPI
18	2313.5	77.9	582	6	Abg74797	Murine DN
19	2313.5	77.9	582	7	Abm04787	Rat Na-de
20	2313.5	77.9	582	7	Abm04787	Rat Na-de
21	2313.5	77.9	582	6	Adc15494	Mouse DNP
22	2307.5	77.7	582	4	Adc15492	Rat DNPI
23	2185	73.6	589	6	Aam79273	Human pro
24	2185	73.6	589	6	Aau99329	Human tra
25	2185	73.6	589	7	Aao30994	Human tra
26	2185	73.6	589	7	Add01392	Human TCH
27	2185	73.6	589	8	Adg88329	Human tra
28	2174.5	73.2	860	5	Adr10021	Human pro
29	2154.5	72.5	601	7	Abb07689	Rat gluta
30	2138.5	72.0	566	7	Add01410	Mouse TCH
31	1980.5	66.7	588	6	Adj95072	Novel NOV
32	1297	43.7	576	8	Aae32079	Human TRI
33	1297	43.7	576	8	Aaw88523	Eat-4 pro
34	1198.5	40.4	560	8	Adn23170	Bacterial
35	1186	39.9	564	7	Adm04596	Human pro
36	1025.5	34.5	204	7	Abb59401	Drosophil
37	986.5	33.2	502	4	Adb64099	Human pro
38	986.5	33.2	502	4	Abb65873	Drosophil
39	971	32.7	573	8	Abb60525	Drosophil
40	971	32.7	573	8	Adn23219	Bacterial
41	950	32.0	544	8	Adn23218	Bacterial
42	940	31.6	495	3	Adn23220	Bacterial
43	940	31.6	495	4	Aay45087	Partial h
44	940	31.6	495	8	Aab66967	Human AST
45	940	31.6	495	8	Adj75516	Marker ge
		31.6	495	8	Adr14587	Human NF-

ALIGNMENTS

RESULT 1
AAW05148

ID   AAW05148 standard; protein; 560 AA.
XX
AC   AAW05148;
XX
DT   30-JAN-1997 (first entry)
XX
DE   Human brain sodium-dependent inorganic phosphate cotransporter.
XX
KW   Brain sodium-dependent inorganic phosphate cotransporter; hBNPI.
XX
OS   Homo sapiens.
XX
PN   WO9634288-A1.
XX
PD   31-OCT-1996.
XX
PF   25-APR-1996; 96WO-US005792.
XX
PR   27-APR-1995; 95US-0043003.
XX
PA   (ELIL) LILLY & CO ELI.
XX
PI   Ni B, Paul SM;
XX
DR   WPI; 1996-497773/49.
DR   N-PSDB; AAT42064.
XX
PT   New isolated human brain sodium-dependent inorganic phosphate co-
PT   transporter - used to develop prods for diagnosis, treatment and
PT   prevention of conditions involving inappropriate stimulation.
XX
PS   Claim 1; Page 55-57; 68pp; English.
XX
CC   A novel human brain sodium-dependent inorganic phosphate cotransporter
CC   (AAW05148), designated hBNPI, is selectively expressed in discrete
CC   populations of neurons and glia. Its amino acid sequence was deduced from
CC   a cDNA clone (AAT42064) isolated from a human hippocampus cDNA library.
CC   hBNPI can be expressed in transformed host cells and used to determine
CC   the effectiveness of test cpds. for the treatment or prevention of
CC   disorders associated with an inappropriate stimulation of hBNPI.
XX
SQ   Sequence 560 AA;

Query Match   100.0%; Score 2970; DB 2; Length 560;
Best Local Similarity   100.0%; Pred. No. 5.2e-267;
Matches 560; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy     1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60

Qy    61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120

Qy   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300

Qy   301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy   361 IADFLRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 IADFLRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy   421 GFNVNHLDIAPRYASILMGISNGVGTLLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GFNVNHLDIAPRYASILMGISNGVGTLLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEARPPGAPPAPPPS 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEARPPGAPPAPPPS 540

Qy   541 YGATHSTFQPPRPPPVRDY 560
         |||||||||||||||||||
Db   541 YGATHSTFQPPRPPPVRDY 560
```

RESULT 2

ABG74792

ID   ABG74792 standard; protein; 560 AA.
XX
AC   ABG74792;
XX
DT   10-JUN-2003 (first entry)
XX
DE   Human BNPI protein #2.
XX
KW   BNPI; sodium-dependent inorganic phosphate cotransporter; DNPI;
KW   pain-regulation; glutamate transport mediator; musculo-skeletal pain;
KW   brain sodium-dependent inorganic phosphate cotransporter; analgesic;
KW   brain inorganic phosphate cotransporter; antimigraine; chronic pain;
KW   differentiation-associated inorganic phosphate cotransporter; migraine;
KW   neuropathy; allodynic pain; mechanical hyperalgesia; diabetic neuropathy;
KW   visceral pain; cerebral pain; peripheral pain; inflammatory pain;
KW   cluster headache; trigeminal neuralgia; enzyme.
XX
OS   Homo sapiens.
XX
PN   WO200210I394-A2.
XX
PD   19-DEC-2002.
XX
PF   13-JUN-2002; 2002WO-EP006484.
XX
PR   13-JUN-2001; 2001DE-01028541.
XX
PA   (CHEF) GRUENENTHAL GMBH.
PI   Weihe E, Schaefer MK;
XX
DR   WPI; 2003-I48835/14.
DR   N-PSDB; ABXI3550.
XX
PT   Identifying pain-regulating compounds, useful particularly for treating
PT   chronic pain, based on interaction with specific phosphate
PT   cotransporters.
XX
PS   Claim 1a; Fig 1d; 104pp; German.
XX
CC   This invention describes a novel method for identifying pain-regulating
CC   substances. The method comprises incubating a test substance with BNPI
CC   (brain sodium-dependent inorganic phosphate cotransporter) or DNPI
CC   (differentiation-associated sodium-dependent inorganic phosphate
CC   cotransporter then measuring either binding of the test substance to BNPI
CC   or DNPI or some functional property of the proteins that is altered by
CC   binding, to the test substance. The novel pain-regulating substances have
CC   analgesic and antimigraine activity. BNPI and DNPI are mediators of
CC   glutamate transport. The products of the invention are used for treating
CC   chronic pain, particularly musculo-skeletal, neuropathic (especially
CC   allodynic pain, mechanical hyperalgesia or diabetic neuropathy),
CC   visceral, cerebral, peripheral and/or inflammatory pain, also migraine,
CC   cluster headache and trigeminal neuralgia. This sequence represents the
CC   human BNPI polypeptide encoded by a polynucleotide (deposited in
CC   AAT420649) which is used in the method disclosed in the invention
XX
SQ   Sequence 560 AA;

Query Match   100.0%; Score 2970; DB 6; Length 560;
Best Local Similarity 100.0%; Pred. No. 5.2e-267;
Matches   560; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy     1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60

Qy    61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120

Qy   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300

Qy   301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy   361 IADFLRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 IADFLRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy   421 GFNVNHLDIAPRYASILMGISNGVGTLLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GFNVNHLDIAPRYASILMGISNGVGTLLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEARPPGAPPAPPPS 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEARPPGAPPAPPPS 540

Qy   541 YGATHSTFQPPRPPPVRDY 560
         |||||||||||||||||||
Db   541 YGATHSTFQPPRPPPVRDY 560
```

RESULT 3

```
AC   ADC15484
XX
ID   ADC15484 standard; protein; 560 AA.
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human BNPI protein #2.
XX
KW   BNPI; DNPI;
KW   brain-associated sodium-dependent inorganic phosphate transporter;
KW   differentiation-associated inorganic phosphate transporter;
KW   ophthalmological; auditory; neuroleptic; antimanic; antidepressant;
KW   cerebroprotective; neuroprotective; analgesic; anorectic; anticonvulsant;
KW   antiparkinsonian; vasotropic; antiemetic; antiarthritic; tranquillizer;
KW   virucide; antibacterial; protozoacide; antiinflammatory; cardiant;
KW   hypotensive; antiasthmatic; immunosuppressive; antidiabetic;
KW   antialcoholic; anti-HIV; nootropic; antiallergic; gene therapy;
KW   vision disorder; retinitis pigmentosa; optical degeneration;
KW   depression; neuralgia; weight regulation; obesity;
KW   sclerosis; neuralgia; weight regulation; obesity;
KW   hearing disorder; tinnitus; Meniere's disease; schizophrenia; mania;
KW   transient ischemic attacks; emesis (e.g. after chemotherapy); dizziness;
KW   amyotrophic lateral sclerosis; neuralgia; paralysis;
KW   anorexia nervosa; epilepsy; hemiballism, Huntington chorea; stress;
KW   Parkinson's disease; cataract; arthritis; hyperactivity;
KW   developmental disorder; rabies; infection; influenza; malaria; CJD;
KW   inflammatory bowel disease; Crohn's disease; hypertension; toxoplasmosis;
KW   asthma; autoimmunity; neuropathy; diabetes; HIV; AIDS;
KW   autonomic disorder; digestive tract disorder; nervous system disorder;
KW   neurodegeneration; Alzheimer's disease; ischemia; encephalitis;
KW   prion disease; demyelinization; multiple sclerosis; retinal degeneration;
KW   glaucoma; nystagmus; retinal detachment; ataxia; memory disorder;
KW   cognitive disorder; stiff-man syndrome; restless leg syndrome; phobia;
KW   sleep disorder; neurotoxicological disease; spinal motor neuron disease;
KW   muscular atrophy; neuroinflammation; fever; taste disorder; food allergy;
KW   aggression; paranoia; neuroendocrine disorder; Tourette syndrome;
KW   sudden infant death syndrome; cardiac infarct; insomnia; amnesia;
KW   multiple sclerosis; jet lag; sexual dysfunction; impotence; priapism;
KW   neuroprotection; enzyme.
XX
OS   Homo sapiens.
XX
XX
CC   PN   WO2003029828-A2.
XX
PD   10-APR-2003.
XX
PF   24-SEP-2002; 2002WO-EP010707.
XX
PR   24-SEP-2001; 2001DE-01047006.
PR   25-SEP-2001; 2001DE-01047028.
XX
PA   (CHEP ) GRUENENTHAL GMBH.
XX
PI   Weihe E,  Schaefer MK;
XX
DR   WPI; 2003-354751/33.
DR   N-PSDB; ADC15483.
XX
PT   Identifying agents for treatment and diagnosis of diseases, e.g.
PT   depression or viral infections, from binding to inorganic phosphate
PT   transporters, also new agents.
XX
PS   Claim 1; Fig 1d; 129pp; German.
XX
CC   This invention describes a novel method of identifying agents for
CC   detection or treatment of specified conditions. The method comprises
CC   incubating test compound with BNPI or DNPI (brain or differentiation-
CC   associated sodium-dependent inorganic phosphate transporter), or related
CC   proteins, nucleic acids or cells (and/or cell preparations), then
CC   measuring binding of test compound or some functional parameter altered
CC   by binding. The products of the invention have ophthalmological,
CC   auditory, neurologic, antimanic, antidepressant, cerebroprotective,
CC   neuroprotective, analgesic, anorectic, anticonvulsant, antiparkinsonian,
CC   vasotropic, antiemetic, antiarthritic, tranquillizer, virucide,
CC   antibacterial, protozoacide, antiinflammatory, cardiant, hypotensive,
CC   antiasthmatic, immunosuppressive, antidiabetic, antialcoholic, anti-HIV,
CC   nootropic and antiallergic activity. The method is used to identify
CC   agents for diagnosis and treatment (including gene therapy) of disorders
CC   of vision; retinitis pigmentosa; optical degeneration; hearing disorders
CC   or loss; tinnitus; Meniere's disease; schizophrenia; mania; depression;
CC   stroke; brain trauma; 'cut-through' paralysis; amyotrophic lateral
CC   sclerosis; neuralgia; weight regulation; obesity; anorexia nervosa;
CC   epilepsy; hemiballism; Huntington chorea; stress; Parkinson's disease;
CC   cataract; arthritis; hyperactivity; developmental disorders; rabies;
CC   bacterial and viral infections; influenza; malaria; CJD; inflammatory
CC   bowel disease; Crohn's disease; hypertension; baroafferent and chemoafferent
CC   functional disorders; hypertension; obesity; anorexia nervosa
CC   diseases; toxoplasmosis; asthma; autoimmunity in central and peripheral
CC   nervous systems; diabetic or alcoholic neuropathy; autoimmune diabetes;
CC   HIV-neuro-AIDS; disorders of the autonomic or digestive tract nervous
CC   systems; overexcitability, particularly mediated by glutamate;
CC   neurodegeneration; Alzheimer's disease; ischemia; encephalitis (viral,
CC   bacterial, Rasmussen or HIV); prion diseases; demyelinization
CC   (particularly multiple sclerosis); retinal degeneration; glaucoma;
CC   nystagmus; retinal detachment; diseases of cerebellum (ataxia); basal
CC   ganglia, pallidum, hearing or balancing organs, auditory canal; memory,
CC   learning and cognitive disorders; stiff-man or restless leg syndromes;
CC   anxiety; phobia; sleep disorders; drug dependency, addiction or
CC   withdrawal (especially alcohol, nicotine, opiates, ecstasy or cocaine);
CC   hepatoencephalopathy; with or without alcohol intoxication;
CC   neurotoxicological diseases; spinal motor neuron diseases; muscular
CC   atrophy or dystrophy; spinal cord disease; neuroinflammation; fever;
CC   taste disorders; food allergies; Chinese restaurant syndrome; aggression;
CC   paranoia; tremors; neuroendocrine disorders; Tourette syndrome;
CC   cerebrovascular spasms; neuronal apoptosis or necrosis; astrocytosis;
CC   burn-out syndrome; sudden infant death syndrome; cardiac infarct;
CC   insomnia; retrograde amnesia; multiple sclerosis; jet lag; sexual
CC   dysfunction (impotence; priapism); also promotion of microglial activity,
CC   learning, cognition or memory; neuroprotection; diagnosis of neurostatic
CC   disease, and as adjuvant therapy for electrostimulation of the
CC   subthalamic nucleus in Parkinson's disease. This sequence represents a
CC   human BNPI protein described in the disclosure of the invention.
XX
SQ   Sequence 560 AA;
```

```
Query Match             100.0%;  Score 2970;  DB 7;  Length 560;
Best Local Similarity   100.0%;
Matches  560;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy          1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCPGLP 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCPGLP 60

Qy         61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120

Qy        121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy        181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy        241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300

Qy        301 SMPVYAIIVANFCRSWTFYLLLISQDPYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SMPVYAIIVANFCRSWTFYLLLISQDPYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy        361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
```

```
Db  361  IADFLRSRRIMSTTNVRKLMNCCGFGMEARTLLLVVGYSHSKGVAISFLVLAVGFSGFAIS
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  361  IADFLRSRRIMSTTNVRKLMNCCGFGMEARTLLLVVGYSHSKGVAISFLVLAVGFSGFAIS  420

Qy  421  GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY  480

Qy  481  GGVIFYGVPASGEKQPWAEPEEMSEEKCCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  GGVIFYGVPASGEKQPWAEPEEMSEEKCCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS  540

Qy  541  YGATHSTFQPPRPPPVRDY  560
         |||||||||||||||||||
Db  541  YGATHSTFQPPRPPPVRDY  560
```

RESULT 4

AAW70500

ID   AAW70500 standard; protein; 560 AA.
XX
AC   AAW70500;
XX
DT   18-JAN-1999   (first entry)
XX
DE   Human sodium-lithium countertransporter BNPI.
XX
KW   Sodium-lithium countertransporter; sodium-phosphate cotransporter; BNPI;
KW   human; lithium therapy; manic depression.
XX
OS   Homo sapiens.
XX
PN   WO983203-A1.
XX
PD   03-SEP-1998.
XX
PF   11-FEB-1998;   98WO-US002875.
PR   27-FEB-1997;   97US-0039462P.
XX
PA   (UYEM-) UNIV EMORY.
XX
PI   Gunn RB,   Timmer RT;
XX
DR   WPI; 1998-520759/44.
DR   N-PSDB; AAV33503.
XX
PT   New isolated lithium-sodium counter-transporter DNA - used to develop
PT   products for evaluating lithium-sodium transport in erythrocytes,
PT   particularly for lithium therapy in manic depression.
XX
PS   Claim 8; Page 45-47; 64pp; English.
XX
CC   This polypeptide comprises the brain-specific human lithium-sodium
CC   countertransporter (LSCT) BNPI. A DNA sequence for human BNPI is provided
CC   (see AAV33503). LSCTs such as BNPI provide the physiological mechanism
CC   for the extrusion of lithium from cells, i.e. it regulates the cell
CC   concentration of lithium. Its activity determines the therapeutic effect
CC   of lithium. The invention provides a simple molecular biological test for
CC   the ability of cells to extrude lithium. The LSCTs have significance for
CC   determining the responsiveness of humans with mental disorders, including
CC   manic depressives, to treatment with lithium salts. Probes and primers
CC   for BNPI, PiT-1 (see AAW70499), PiT-2 (see AAW70498) can be used in
CC   diagnostic tests useful for genetic screenings to predict whether a
CC   patient will respond to lithium treatment. The test is also a screen for
CC   susceptibility to, and extent of, manic depressive illness, and is
CC   suitable for screening newborns
XX
SQ   Sequence 560 AA;

Query Match   99.8%;   Score 2967; DB 2; Length 560;
Best Local Similarity   99.8%;
Matches 559; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

                                 Score 2967; DB 2; Length 560;
                         Pred. No. 9.9e-267;
```

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```
Qy    1  MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP  60
         ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db    1  MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETVELSADGRPVTTQTRDPPVVDCTCFGLP  60

Db   61  RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   61  RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH  120

Qy  121  GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQ  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQ  180

Db  181  LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  181  LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV  240

Qy  241  YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFT  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  YGSFGIFWLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFT  300

Db  301  SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  301  SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ  360

Qy  361  IADFLRSRRIMSTTNVRKLMNCCGFGMEARTLLLVVGYSHSKGVAISFLVLAVGFSGFAIS  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  IADFLRSRRIMSTTNVRKLMNCCGFGMEARTLLLVVGYSHSKGVAISFLVLAVGFSGFAIS  420

Db  421  GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  421  GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY  480

Qy  481  GGVIFYGVPASGEKQPWAEPEEMSEEKCCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  GGVIFYGVPASGEKQPWAEPEEMSEEKCCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS  540

Qy  541  YGATHSTFQPPRPPPVRDY  560
         |||||||||||||||||||
Db  541  YGATHSTFQPPRPPPVRDY  560
```

RESULT 5

ABG74791

ID   ABG74791 standard; protein; 560 AA.
XX
AC   ABG74791;
XX
DT   10-JUN-2003   (first entry)
XX
DE   Human BNPI protein.
XX
KW   BNPI; sodium-dependent inorganic phosphate cotransporter; DNPI;
KW   pain-regulation; glutamate transport mediator; musculo-skeletal pain;
KW   brain sodium-dependent inorganic phosphate cotransporter; analgesic;
KW   brain inorganic phosphate cotransporter; antimigraine; chronic pain;
KW   differentiation-associated inorganic phosphate cotransporter; migraine;
KW   neuropathy; allodynic pain; mechanical hyperalgesia; diabetic neuropathy;
KW   visceral pain; cerebral pain; peripheral pain; inflammatory pain;
KW   cluster headache; trigeminal neuralgia; PIM-1 kinase; enzyme.
XX
OS   Homo sapiens.
XX
PN   WO2002101394-A2.
XX
PD   19-DEC-2002.
XX
PF   13-JUN-2002;   2002WO-EP006484.
PR   13-JUN-2001;   2001DE-01028541.
XX
PA   (CHEF) GRUENENTHAL GMBH.
XX
PI   Weihe E,   Schaefer MK;

```
XX
DR  WPI; 2003-148835/14.
DR  N-PSDB; ABX13549.
XX
PS  Claim 1a; Fig 1b; 104pp; German.
XX
PT  cotransporters.
PT  chronic pain, based on interaction with specific phosphate
PT  Identifying pain-regulating compounds, useful particularly for treating
XX
CC  disclosed in the invention
CC  polynucleotide deposited in NM_020309 which is used in the method
CC  human BNPI polypeptide (also described as PIM-1 kinase) encoded by a
CC  cluster headache and trigeminal neuralgia. This sequence represents the
CC  visceral, cerebral, peripheral and/or inflammatory pain, also migraine,
CC  allodynic pain, mechanical hyperalgesia or diabetic neuropathy),
CC  chronic pain, particularly musculo-skeletal, neuropathic (especially
CC  hypotensive; antiasthmatic; immunosuppressive; antidiabetic;
CC  glutamate transport. The products of the invention are used for treating
CC  analgesic and antimigraine activity. BNPI and DNPI are mediators of
CC  binding to the test substance to BNPI
CC  or DNPI or some functional property of the proteins that is altered by
CC  cotransporter then measuring either binding of the test substance to ENPI
CC  (differentiation-associated sodium-dependent inorganic phosphate
CC  (brain sodium-dependent inorganic phosphate cotransporter) or DNPI
CC  substances. The method comprises incubating a test substance with BNPI
CC  This invention describes a novel method for identifying pain-regulating
XX
SQ  Sequence 560 AA;
XX
CC
CC  Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC  Best Local Similarity 99.8%; Pred. No. 2.9e-266;
CC  Query Match 99.7%; Score 2962; DB 6; Length 560;
XX

Qy    1 MEFRQEEFRKLAGRALGKLIHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MEFRQEEFRKLAGRALGKLIHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60

Qy   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGHVVVQKAQFSWDPETVGLIH 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGHVVVQKAQFSWDPETVGLIH 120

Qy  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300

Qy  301 SMPVYAIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SMPVYAIVANFCRSWTFYLLLISQPAYFEEVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 360

Qy  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy  421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy  481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEEPGAPAPPPS 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEEPGAPAPPPS 540

Qy  541 YGATHSTFQPPRPPPVRDY 560
         ||||||||||||||||||||
Db  541 YGATHSTFQPPRPPPVRDY 560
```

```
ID  ADC15482 standard; protein; 560 AA.
XX
AC  ADC15482;
XX
DT  18-DEC-2003 (first entry)
XX
DE  Human BNPI protein #1.
XX
KW  BNPI; DNPI; brain-associated sodium-dependent inorganic phosphate transporter;
KW  differentiation-associated sodium-dependent inorganic phosphate transporter;
KW  ophthalmological; auditory; neuroleptic; antimanic; antidepressant;
KW  cerebroprotective; neuroprotective; analgesic; anorectic; anticonvulsant;
KW  antiparkinsonian; vasotropic; antiemetic; antiarthritic; tranquillizer;
KW  virucide; antibacterial; protozoacide; antiinflammatory; cardiant;
KW  antialcoholic; anti-HIV; nootropic; antiallergic; gene therapy;
KW  hypotensive; antiasthmatic; immunosuppressive; antidiabetic;
KW  vision disorder; retinitis pigmentosa; optical degeneration;
KW  hearing disorder; tinnitus; Meniere's disease; schizophrenia; mania;
KW  depression; stroke; brain trauma; paralysis;
KW  amyotrophic lateral sclerosis; neuralgia; weight regulation; obesity;
KW  anorexia nervosa; epilepsy; hemibalism; Huntington chorea; stress;
KW  Parkinson's disease; cataract; arthritis; hyperactivity;
KW  developmental disorder; rabies; infection; influenza; malaria; CJD;
KW  inflammatory bowel disease; Crohn's disease; hypertension; toxoplasmosis;
KW  asthma; autoimmunity; neuropathy; diabetes; HIV; AIDS;
KW  autonomic disorder; digestive tract disorder; nervous system disorder;
KW  neurodegeneration; Alzheimer's disease; ischemia; encephalitis;
KW  prion disease; demyelinization; multiple sclerosis; retinal degeneration;
KW  glaucoma; nystagmus; retinal detachment; ataxia; memory disorder;
KW  cognitive disorder; stiff-man syndrome; restless leg syndrome; phobia;
KW  sleep disorder; neurotoxicological disease; spinal motor neuron disease;
KW  muscular atrophy; neuroinflammation; fever; taste disorder; food allergy;
KW  aggression; paranoia; neuroendocrine disorder; Tourette syndrome;
KW  sudden infant death syndrome; cardiac infarct; insomnia; amnesia;
KW  multiple sclerosis; jet lag; sexual dysfunction; impotence; priapism;
KW  neuroprotection; enzyme.
XX
OS  Homo sapiens.
XX
PN  WO200302928-A2.
XX
PD  10-APR-2003.
XX
PF  24-SEP-2002; 2002WO-EP010707.
XX
PR  24-SEP-2001; 2001DE-01047006.
PR  25-SEP-2001; 2001DE-01047028.
XX
PA  (CHEF ) GRUENENTHAL GMBH.
XX
PI  Weihe E, Schaefer MK;
XX
DR  WPI; 2003-354751/33.
XX
PS  Claim 1; Fig 1b; 129pp; German.
XX
PT  transporters, also new agents.
PT  depression or viral infections, from binding to inorganic phosphate
PT  Identifying agents for treatment and diagnosis of diseases, e.g.
XX
CC  neuroprotective, analgesic, anorectic, anticonvulsant, antiparkinsonian,
CC  auditory, neuroleptic, antimanic, antidepressant, cerebroprotective,
CC  by binding. The products of the invention have ophthalmological,
CC  measuring binding of the test compound or some functional parameter altered
CC  proteins, nucleic acids or cells (and/or cell preparations), then
CC  associated sodium-dependent inorganic phosphate transporter), or related
CC  incubating test compound with BNPI or DNPI (brain or differentiation-
CC  detection or treatment of specified conditions. The method comprises
CC  This invention describes a novel method of identifying agents for
```

CC   vasotropic, antiemetic, antiarthritic, tranquillizer, virucide,
CC   antibacterial, protozoacide, antiinflammatory, cardiant, hypotensive,
CC   antiasthmatic, immunosuppressive, antidiabetic, antialcoholic, anti-HIV,
CC   nootropic and antiallergic activity. The method is used to identify
CC   agents for diagnosis and treatment (including gene therapy) of disorders
CC   of vision; retinitis pigmentosa; optical degeneration; hearing disorders
CC   or loss; tinnitus; Meniere's disease; schizophrenia; mania; depression;
CC   stroke; brain trauma; 'cut-through' paralysis; amyotrophic lateral
CC   sclerosis; neuralgia; weight regulation; obesity; anorexia nervosa;
CC   epilepsy; hemibalism; Huntington chorea; Parkinson's disease;
CC   transient ischemic attacks; emesis (e.g. after chemotherapy); dizziness;
CC   bacterial and viral infections; influenza; malaria; CJD; inflammatory
CC   bowel disease; Crohn's disease; cardio-vascular and -respiratory
CC   functional disorders; hypertension; baroafferent and chemoafferent
CC   diseases; toxoplasmosis; asthma; autoimmunity in central and peripheral
CC   nervous systems; diabetic or alcoholic neuropathy; autoimmune diabetes;
CC   HIV-neuro-AIDS; disorders of the autonomic or digestive tract nervous
CC   systems; overexcitability, particularly mediated by glutamate;
CC   neurodegeneration; Alzheimer's disease; ischemia; encephalitis (viral,
CC   bacterial, Rasmussen or HIV); prion diseases; demyelinization
CC   (particularly multiple sclerosis); retinal degeneration; glaucoma;
CC   nystagmus; retinal detachment; diseases of cerebellum (ataxia; basal
CC   ganglia, pallidum, hearing or balancing organs, auditory canal; memory,
CC   learning and cognitive disorders; stiff-man or restless leg syndromes;
CC   anxiety; phobia; sleep disorders; drug dependency, addiction or
CC   withdrawal (especially alcohol, nicotine, opiates, ecstasy or cocaine);
CC   hepatoencephalopathy, with or without alcohol intoxication;
CC   neurotoxicological diseases; spinal motor neuron diseases; muscular
CC   atrophy or dystrophy; spinal cord disease; neuroinflammation; fever;
CC   taste disorders; food allergies; Chinese restaurant syndrome; aggression;
CC   paranoia; tremors; neuroendocrine disorders; Tourette syndrome;
CC   cerebrovascular spasms; neuronal apoptosis or necrosis; astrocytosis;
CC   burn-out syndrome; sudden infant death syndrome; cardiac infarct;
CC   insomnia; retrograde amnesia; multiple sclerosis; jet lag; sexual
CC   dysfunction (impotence; priapism); also promotion of neurostatic
CC   disease, and as adjuvant therapy for electrostimulation of the
CC   learning, cognition or memory; neuroprotection; diagnosis of neurostatic
CC   subthalamic nucleus in Parkinson's disease. This sequence represents the
CC   human BNPI protein also represented in AN: NM_020309.
XX
SQ   Sequence 560 AA;

Query Match   99.7%;   Score 2962;   DB 7;   Length 560;
Best Local Similarity   99.8%;
Matches 559;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Qy   1   MEFRQEEFRKLAGRALGKLHRILEKROEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP   60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1   MEFRQEEFRKLAGRALGKLHRILEKROEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP   60

Qy   61   RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH   120
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61   RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH   120

Qy   121   GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG   180
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121   GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG   180

Qy   181   LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSSVFV   240
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181   LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSSVFV   240

Qy   241   YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT   300
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241   YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT   300

Qy   301   SMPVYAIIVANFCRSWTFYLLLISQPDVYFEEVPGFEISKVGLYSALPHVMTIIVPIGGQ   360
       |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   301   SMPVYAIIVANFCRSWTFYLLLISQPAVYFEEVPGFEISKVGLVSALPHVMTIIVPIGGQ   360

Qy   361   IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVIAVGFSGFAIS   420
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361   IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVIAVGFSGFAIS   420

Qy   421   GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY   480
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421   GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY   480

Qy   481   GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS   540
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481   GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS   540

Qy   541   YGATHSTFQPPRPPPPVRDY   560
       ||||||||||||||||||||
Db   541   YGATHSTFQPPRPPPPVRDY   560

RESULT 7
ADD01474

ID   ADD01474 standard; protein; 560 AA.
XX
AC   ADD01474;
XX
DT   01-JAN-2004   (first entry)
XX
DE   Human VGLUT1 protein sequence.
XX
KW   antidiabetic; antilipemic; antiarteriosclerotic; nootropic;
KW   neuroprotective; anabolic; antiinflammatory; immunosuppressive;
KW   cytostatic; antiasthmatic; antiarthritic; cerebroprotective;
KW   antiallergic; dermatological; cardiant; antiParkinsonian; neuroleptic;
KW   glucose transporter; potassium ion channel protein; diabetes;
KW   hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;
KW   colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;
KW   sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;
KW   meningitis; hepatitis; myocarditis; asthma; immune disorder;
KW   multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;
KW   allergy; hay fever; allergic rhinitis; anaphylactic shock;
KW   atopic dermatitis; circulatory disorder; heart failure; cancer;
KW   Alzheimer's disease; Parkinson's disease; schizophrenia;
KW   hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.
XX
OS   Homo sapiens.
XX
FN   WO200305419O-A1.
XX
PD   03-JUL-2003.
XX
PF   19-DEC-2002; 2002WO-JP013290.
XX
PR   21-DEC-2001; 2001JP-00389361.
PR   25-DEC-2001; 2001JP-00392577.
PR   26-DEC-2001; 2001JP-00394947.
PR   26-DEC-2001; 2001JP-00395467.
PR   06-FEB-2002; 2002JP-00030010.
PR   08-FEB-2002; 2002JP-00033095.
PR   06-JUN-2002; 2002JP-00165336.
XX
PA   (TAKE) TAKEDA CHEM IND LTD.
XX
PI   Nakanishi A,   Sagiya Y,   Uno Y;
XX
DR   WPI; 2003-541817/51.
XX
PT   Glucose transporter TCH099, vesicular glutamate transporter TCH177 and
PT   potassium channel protein TCH136 and DNA encoding them for diagnosis,
PT   treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and
PT   digestive disorders.
XX
PS   Disclosure; Fig 3; 221pp; Japanese.
XX
CC   The invention relates to a novel glucose transporter TCH099, vesicular
CC   glutamate transporter TCH177 and voltage-dependent potassium ion channel
CC   protein TCH136. The sequences are useful in the treatment, prevention and
CC   diagnosis of a broad range of diseases including diabetes, hyperlipemia,

CC   arteriosclerosis, digestive disorders (such as Crohn's disease, colitis,
CC   gastritis, ileitis and rectal inflammation), inflammatory diseases,
CC   sepsis, prostatic hypertrophy, reproductive disorders, pneumonia,
CC   meningitis, hepatitis, myocarditis, pneumonia, immune disorders (such as
CC   multiple sclerosis, rheumatoid arthritis, asthma, anaphylactic shock and
CC   allergies (such as hay fever, allergic rhinitis, Sjogren's disease and lupus),
CC   atopic dermatitis), circulatory disorders (such as heart failure), cancer
CC   (such as cancer of the lung, kidney, liver, ovary, prostate, stomach,
CC   pancreas, bladder, breast, fallopian tubes or colon), central nervous
CC   system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and
CC   secretory disorders (such as hyperprolactinemia and Cushing's disease). This
CC   sequence represents the protein sequence for the human VGLUT1 glutamate
CC   transporter which was used for comparison with the novel human vesicular
CC   glutamate transporter TCH177.
XX
SQ   Sequence 560 AA;

Query Match   99.7%; 99.8%; Score 2962; DB 7; Length 560;
Best Local Similarity
Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 MEFRQEEFRKLAGRALGKLIHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MEFRQEEFRKLAGRALGKLIHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60

Qy   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120

Qy   121 GSFFWGYIVTQIPGGFICQKFAANRVGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GSFFWGYIVTQIPGGFICQKFAANRVGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSSVFYV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSSVFYV 240

Qy   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300

Qy   301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   301 SMPVYAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy   361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy   421 GPNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GPNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy   481 GGVIFYGVPASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540

Qy   541 YGATHSTFQPPRPPPPEVRDY 560
          |||||||||||||||||||||
Db   541 YGATHSTFQPPRPPPPEVRDY 560

RESULT 8
AA013870
ID   AA013870 standard; protein; 567 AA.
XX
AC   AA013870;
XX
DT   06-NOV-2001 (first entry)
XX
DE   Human polypeptide SEQ ID NO 27762.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorders; arthritis; inflammation.
XX
OS   Homo sapiens.
XX
FH
PN   WO200164835-A2.
XX
PN   WO200164835-A2.
XX
PD   07-SEP-2001.
XX
PF   26-FEB-2001; 2001WO-US004927.
XX
PR   28-FEB-2000; 2000US-00515126.
PR   18-MAY-2000; 2000US-00577409.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Liu C, Drmanac RT;
XX
DR   WPI; 2001-514838/56.
DR   N-PSDB; AA193801.
XX
PT   Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT   and treating e.g. leukemia, inflammation and immune disorders.
XX
PS   Claim 20; SEQ ID NO 27762; 1399pp + Sequence Listing; English.
XX
CC   The invention relates to human polynucleotides (AA179941-AA193841) and
CC   the encoded proteins (AA000010-AA013910) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and/or
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation. Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 567 AA;

Query Match   99.7%; 99.8%; Score 2962; DB 4; Length 567;
Best Local Similarity
Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 MEFRQEEFRKLAGRALGKLIHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8 MEFRQEEFRKLAGRALGKLIHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 67

Qy   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   68 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 127

Qy   121 GSFFWGYIVTQIPGGFICQKFAANRVGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   128 GSFFWGYIVTQIPGGFICQKFAANRVGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 187

Qy   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSSVFYV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   188 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSSVFYV 247

Qy   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   248 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 307

Qy   301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
          ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   308 SMPVYAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 367

Qy   361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Db   368 IADFLRSRRIMSTTNVRKLMNCGFGMEATLLIVGYSHSKGVAISFLVLAVGFSGFAIS 427

Qy   421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Db   428 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 487

Qy   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540

Db   488 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 547

Qy   541 YGATHSTFQPPRPPPPVRDY 560

Db   548 YGATHSTPQPPRPPPPVRDY 567

RESULT 9

ID   ABG74794 standard; protein; 560 AA.
AC   ABG74794;
DT   10-JUN-2003 (first entry)
DE   Murine BNP1 protein.
KW   BNP1; sodium-dependent inorganic phosphate cotransporter; DNPI;
KW   pain-regulation; glutamate transport mediator; musculo-skeletal pain;
KW   brain sodium-dependent inorganic phosphate cotransporter; analgesic;
KW   brain inorganic phosphate cotransporter; antimigraine; chronic pain;
KW   differentiation-associated inorganic phosphate cotransporter; migraine;
KW   neuropathy; allodynic pain; mechanical hyperalgesia; diabetic neuropathy;
KW   visceral pain; cerebral pain; peripheral pain; inflammatory pain; murine;
KW   cluster headache; trigeminal neuralgia; enzyme.
OS   Mus musculus.
PN   WO200210139A-A2.
PD   19-DEC-2002.
PF   13-JUN-2002; 2002WO-EP006484.
PR   13-JUN-2001; 2001DE-01028541.
PA   (CHEF) GRUENENTHAL GMBH.
PI   Weihe E, Schaefer MK;
DR   WPI; 2003-148835/14.
DR   N-PSDB; ABX13552.
PT   Identifying pain-regulating compounds, useful particularly for treating
PT   chronic pain, based on interaction with specific phosphate
PT   cotransporters.
PS   Claim 1a; Fig 1h; 104pp; German.
CC   This invention describes a novel method for identifying pain-regulating
CC   substances. The method comprises incubating a test substance with BNPI
CC   (brain sodium-dependent inorganic phosphate cotransporter) or DNPI
CC   (differentiation-associated sodium-dependent inorganic phosphate
CC   cotransporter) then measuring either binding of the proteins to BNPI
CC   or DNPI or some functional property of the proteins that is altered by
CC   binding to the test substance. The novel pain-regulating substances have
CC   analgesic and antimigraine activity. BNPI and DNPI are mediators of
CC   glutamate transport. The products of the invention are used for treating
CC   chronic pain, particularly musculo-skeletal, neuropathic (especially
CC   allodynic pain, mechanical hyperalgesia or diabetic neuropathy),
CC   visceral, cerebral, peripheral and/or inflammatory pain, also migraine,
CC   cluster headache and trigeminal neuralgia. This sequence represents
CC   murine BNP1 polypeptide encoded by the polynucleotide (deposited in
CC   XM_133432) used in the method disclosed in the invention

SQ   Sequence 560 AA;

Query Match   98.6%;   Score 2929; DB 6; Length 560;
Best Local Similarity   98.4%;   Pred. No. 3.4e-263;
Matches 551; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy   1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
          |||||||||:||||||||||||||::||||||||:||||||||||||:|||||||||||||
Db   1 MEFRQEEFRKLAGRALGRLLHRLLEKRQEGAETLELSADGRPVTTHTRDPPVVDCTCFGLP 60

Qy   61 RRYIIAIMSGLGFCLISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPEVGLIH 120
          |||||||||||||||:||||||||||||||||||:||||||||||||||:|||:|||||||
Db   61 RRYIIAIMSGLGFCLISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFNWDPEFVGLIH 120

Qy   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
          ||||||||:|||||||||||||||||||||:|||||||||||||||||||||||||||||
Db   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy   181 LVEGVTYPACHGIWSKWAPPLERSRLAATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 LVEGVTYPACHGIWSKWAPPLERSRLAATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy   241 YGSFGIFWYLFWLLVSYSPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
          ||||||||||||||||||||||||||||:|||||||||:||||||:||||:||||||||
Db   241 YGSFGIFWYLFWLLVSYSPALHPSISEEERKYIEDAIGBSAKLMNPVTKFNTMPWRRFFT 300

Qy   301 SMPVYAIIVANFCRSWTFYLILISQPDYPEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360
          ||||||||||||:|||:|||||||:||||||||||:|||||||||||:||:|||||||||
Db   301 SMPVYAIIVANFCRSWTFYLILISQPAYPEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy   361 IADFLRSRRIMSTTNVRKLMNCGFGMEATLLIVGYSHSKGVAISFLVLAVGFSGFAIS 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 IADFLRSRRIMSTTNVRKLMNCGFGMEATLLIVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy   421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540

Qy   541 YGATHSTFQPPRPPPPVRDY 560
          ||||||||||||||||||||
Db   541 YGATHSTVQPPRPPPPVRDY 560

RESULT 10

ID   ADC15488 standard; protein; 560 AA.
AC   ADC15488;
DT   18-DEC-2003 (first entry)
DE   Mouse BNP1 protein.
KW   BNP1; DNPI;
KW   brain-associated sodium-dependent inorganic phosphate transporter;
KW   differentiation-associated inorganic phosphate transporter;
KW   ophthalmological; auditory; neuroleptic; antimanic; antidepressant;
KW   cerebroprotective; neuroprotective; analgesic; anorectic; anticonvulsant;
KW   antiparkinsonian; vasotropic; antiemetic; antiarthritic; tranquillizer;
KW   virucide; antibacterial; protozoacide; antiinflammatory; cardiant;
KW   hypotensive; antiasthmatic; immunosuppressive; antidiabetic;
KW   antialcoholic; anti-HIV; nootropic; antiallergic; gene therapy;
KW   vision disorder; retinitis pigmentosa; optical degeneration; mania;
KW   hearing disorder; tinnitus; Meniere's disease; schizophrenia;
KW   depression; stroke; brain trauma; paralysis;
KW   amyotrophic lateral sclerosis; neuralgia; weight regulation; obesity;
KW   anorexia nervosa; epilepsy; hemiballism; Huntington chorea; stress;
KW   Parkinson's disease; cataract; arthritis; hyperactivity;
KW   developmental disorder; rabies; infection; influenza; malaria; CJD;

KW inflammatory bowel disease; Crohn's disease; hypertension; toxoplasmosis;
KW asthma; autoimmunity; neuropathy; diabetes; HIV; AIDS;
KW autonomic disorder; digestive tract disorder; nervous system disorder;
KW prion disease; demyelination; Alzheimer's disease; ischemia; encephalitis;
KW neurodegeneration; Alzheimer's disease; multiple sclerosis; retinal degeneration;
KW glaucoma; nystagmus; retinal detachment; ataxia; memory disorder;
KW cognitive disorder; stiff-man syndrome; restless leg syndrome; phobia;
KW sleep disorder; neurotoxicological disease; spinal motor neuron disease;
KW muscular atrophy; neuroinflammation; fever; taste disorder; food allergy;
KW aggression; paranoia; neuroendocrine disorder; Tourette syndrome;
KW sudden infant death syndrome; cardiac infarct; insomnia; amnesia;
KW multiple sclerosis; jet lag; sexual dysfunction; impotence; priapism;
KW neuroprotection; enzyme.
XX
OS Mus sp.
XX
PN WO200329828-A2.
XX
PD 10-APR-2003.
XX
PF 24-SEP-2002; 2002WO-EP010707.
XX
PR 24-SEP-2001; 2001DE-01047006.
PR 25-SEP-2001; 2001DE-01047028.
XX
PA (CHEF) GRUENENTHAL GMBH.
XX
PI Weihe E, Schaefer MK;
XX
PT (CHEF) GRUENENTHAL GMBH.
XX
Claim 1; Fig 1h; 129pp; German.

DR WPI; 2003-354751/33.
XX
PT Identifying agents for treatment and diagnosis of diseases, e.g.
PT depression or viral infections, from binding to inorganic phosphate
PT transporters, also new agents.
XX
PS Claim 1; Fig 1h; 129pp; German.

CC This invention describes a novel method of identifying agents for
CC detection or treatment of specified conditions. The method comprises
CC incubating test compound with BNPI or DNPI (brain or differentiation-
CC associated sodium-dependent inorganic phosphate transporter), or related
CC proteins, nucleic acids or cells (and/or cell preparations), then
CC measuring binding of test compound or some functional parameter altered
CC by binding. The products of the invention have ophthalmological,
CC auditory, neuroleptic, antimanic, antidepressant, cerebroprotective,
CC neuroprotective, analgesic, anorectic, anticonvulsant, antiparkinsonian,
CC vasotropic, antiemetic, antiarthritic, tranquilliser, virucide,
CC antibacterial, protozoacide, antiinflammatory, cardiant, hypotensive,
CC antiasthmatic, immunosuppressive, antidiabetic, antialcoholic, anti-HIV,
CC nootropic and antiallergic activity. The method is used to identify
CC agents for diagnosis and treatment (including gene therapy) of disorders
CC of vision; retinitis pigmentosa; optical degeneration; hearing disorders
CC or loss; tinnitus; Meniere's disease; schizophrenia; mania; depression;
CC stroke; brain trauma; 'cut-through' paralysis; amyotrophic lateral
CC sclerosis; neuralgia; weight regulation; obesity; anorexia nervosa;
CC epilepsy; hemiballism; Huntington chorea; stress; Parkinson's disease;
CC transient ischemic attacks; emesis (e.g. after chemotherapy); dizziness;
CC cataract; arthritis; hyperactivity; developmental disorders; rabies;
CC bacterial and viral infections; influenza; malaria; CJD; inflammatory
CC bowel disease; Crohn's disease; cardio-vascular and -respiratory
CC functional disorders; hypertension; baroafferent and chemoafferent
CC diseases; toxoplasmosis; asthma; autoimmunity in central and peripheral
CC nervous systems; diabetic or alcoholic neuropathy; autoimmune diabetes;
CC HIV-neuro-AIDS; disorders of the autonomic or digestive tract nervous
CC systems; overexcitability, particularly mediated by glutamate;
CC neurodegeneration; Alzheimer's disease; ischemia; encephalitis (viral,
CC bacterial, Rasmussen or HIV); prion diseases; demyelination
CC (particularly multiple sclerosis); retinal degeneration (glaucoma;
CC nystagmus; retinal detachment; diseases of cerebellum (ataxia); basal
CC ganglia, pallidum, hearing or balancing organs, auditory canal; memory,
CC learning and cognitive disorders; stiff-man or restless leg syndromes;
CC anxiety; phobia; sleep disorders; drug dependency, addiction or
CC withdrawal (especially alcohol, nicotine, opiates, ecstasy or cocaine);

CC hepatoencephalopathy, with or without alcohol intoxication;
CC neurotoxicological diseases; spinal motor neuron diseases; muscular
CC atrophy or dystrophy; food allergies; spinal cord disease; neuroinflammation; fever;
CC taste disorders; food allergies; Chinese restaurant syndrome; aggression;
CC paranoia; tremors; neuroendocrine disorders; Tourette syndrome;
CC cerebrovascular spasms; neuronal apoptosis or necrosis; astrocytosis;
CC burn-out syndrome; sudden infant death syndrome; cardiac infarct;
CC insomnia; retrograde amnesia; multiple sclerosis; jet lag; sexual
CC dysfunction (impotence; priapism); also promotion of microglial activity,
CC learning, cognition or memory; neuroprotection; diagnosis of neurostatic
CC disease, and as adjuvant therapy for electrostimulation of the
CC subthalamic nucleus in Parkinson's disease. This sequence represents the
CC mouse BNPI protein also represented in AN: XM_133432.
XX
SQ Sequence 560 AA;

Query Match 98.6%; Score 2929; DB 7; Length 560;
Best Local Similarity 98.4%; Pred. No. 3.4e-263;
Matches 551; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

```
Qy    1 MEFRQEEFRKLAGRALGKLHRLLEKROEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
          ||||||||||||||||| |||||||||||||||||||||||||| ||||||||||||||
Db    1 MEFRQEEFRKLAGRALGRLHRLLEKROEGAETLELSADGRPVTTHTRDPPVVDCTCFGLP 60

Qy   61 RRYIIAIMSGLGFCISFGICRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDEPETVGLIH 120
          |||||||||||| ||||| ||||||||||||||||||||||||||||| ||| |||||||
Db   61 RRYIIAIMSGLGRCISFGTRCNLGVAIVSMVNNSTTHRGGHVVVQKAQPNWDPETVGLIH 120

Qy  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
          |||||||||||||||||||||||||||||||||||||||||||||| |||| |||||||
Db  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPVTKFNTPWRRFFT 300

Qy  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360
          ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  301 SMPVYAIIVANFCRSWTFYLLLISQPAYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFIVLAVGFSGFAIS 420
          |||||||| |||||||| ||||| |||||||||||||||||||||||||||||||||||
Db  361 IADFLRSRHIMSTTNVRLMNCCGFGMEATLLLVVGYSHSKGVAISFIVLAVGFSGFAIS 420

Qy  421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy  481 GGVIFYGVPASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPS 540
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db  481 GGVIFYGVPASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSSEMEDEAEPPGAPPAPPS 540

Qy  541 YGATHSTFQPPRPPPVRDY 560
          ||||||| |||||||||||
Db  541 YGATHSTVQPPRPPPVRDY 560
```

RESULT 11
ABG74793
ID ABG74793 standard; protein; 560 AA.
XX
AC ABG74793;
XX
DT 10-JUN-2003 (first entry)
XX
DE Rat BNPI protein.
XX
KW BNPI; sodium-dependent inorganic phosphate cotransporter; DNPI;
KW pain-regulation; glutamate transport mediator; musculo-skeletal pain;

```
KW   brain sodium-dependent inorganic phosphate cotransporter; analgesic;
KW   brain inorganic phosphate cotransporter; antimigraine; chronic pain;
KW   differentiation-associated inorganic phosphate cotransporter; migraine;
KW   neuropathy; allodynic pain; mechanical hyperalgesia; diabetic neuropathy;
KW   visceral pain; cerebral pain; peripheral pain; inflammatory pain; rat;
KW   cluster headache; trigeminal neuralgia; enzyme.
XX
OS   Rattus norvegicus.
XX
PN   WO200210139394-A2.
XX
PD   19-DEC-2002.
XX
PF   13-JUN-2002; 2002WO-EP006484.
XX
PR   13-JUN-2001; 2001DE-01028541.
XX
PA   (CHEF ) GRUENENTHAL GMBH.
XX
PI   Weihe E, Schaefer MK;
XX
DR   WPI; 2003-148835/14.
DR   N-PSDB; ABX13551.
XX
PT   Identifying pain-regulating compounds, useful particularly for treating
PT   chronic pain, based on interaction with specific phosphate
PT   cotransporters.
XX
PS   Claim 1a; Fig 1f; 104pp; German.
XX
CC   This invention describes a novel method for identifying pain-regulating
CC   substances. The method comprises incubating a test substance with BNPI
CC   (brain sodium-dependent inorganic phosphate cotransporter) or DNPI
CC   (differentiation-associated inorganic phosphate cotransporter)
CC   cotransporter then measuring either binding of the proteins that is altered by
CC   or DNPI or some functional property of the proteins that is altered by
CC   binding to the test substance. The novel pain-regulating substances have
CC   analgesic and antimigraine activity. BNPI and DNPI are mediators of
CC   glutamate transport. The products of the invention are used for treating
CC   chronic pain, particularly musculo-skeletal, neuropathic (especially
CC   allodynic pain, mechanical hyperalgesia or diabetic neuropathy),
CC   visceral, cerebral, peripheral and/or inflammatory pain, also migraine,
CC   cluster headache and trigeminal neuralgia. This sequence represents the
CC   rat BNP1 polypeptide encoded by the polynucleotide (deposited in U07609)
CC   which is used in the method disclosed in the invention
XX
SQ   Sequence 560 AA;

Query Match     98.5%;  Score 2925;  DB 6;  Length 560;
Best Local Similarity   98.2%;  Pred. No. 8e-263;
Matches  550;  Conservative   5;  Mismatches   5;  Indels   0;  Gaps   0;

Qy      1 MEFRQEEFRKLAGRALGKHLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
          |||||||||||||||||| |||||||||||||||||||||||||| ||||||||||||||
Db      1 MEFRQEEFRKLAGRALGRLHRLLEKRQEGAETLELSADGRPVTTHTRDPPVVDCTCFGLP 60

Qy     61 RRYIIAIMSGLGFCISFGICRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db     61 RRYIIAIMSGLGFCISFGICRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFNWDPETVGLIH 120

Qy    121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy    181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCCSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCCSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy    241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||| |||
Db    241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPVTKFNTPWRRFFT 300

Qy    301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy    361 IADFLRSRHIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 IADFLRSRHIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy    421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy    481 GGVIFYGVFASGEKQPWAEPEEMSEEKKCCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
          ||||||||||||||||||||||||||||||||||||||||||| |||||| |||||||||||
Db    481 GGVIFYGVFASGEKQPWAEPEEMSEEKKCCGFVGHDQLAGSDESEMEDEVEPPGAPPAPPPS 540

Qy    541 YGATHSTVQPPRPPPPVVRDY 560
          |||||||||||||||||||||
Db    541 YGATHSTVQPPRPPPPVVRDY 560
```

```
RESULT 12
ID   ADC15486
     ADC15486 standard; protein; 560 AA.
XX
AC   ADC15486;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Rat BNP1 protein.
XX
KW   BNP1; DNPI;
KW   brain-associated sodium-dependent inorganic phosphate transporter;
KW   differentiation-associated inorganic phosphate transporter;
KW   ophthalmological; auditory; neuroprotective; antiemetic; antidepressant;
KW   cerebroprotective; neuroprotective; analgesic; antimanic; antidepressant;
KW   antiparkinsonian; vasotropic; antiemetic; antiarthritic; anticonvulsant;
KW   vitucide; antibacterial; protozoacide; antiinflammatory; cardiant;
KW   hypotensive; antiasthmatic; immunosuppressive; antidiabetic;
KW   antialcoholic; anti-HIV; nootropic; antiallergic; gene therapy;
KW   vision disorder; retinitis pigmentosa; optical degeneration;
KW   hearing disorder; tinnitus; Meniere's disease; schizophrenia; mania;
KW   depression; stroke; brain trauma; paralysis;
KW   amyotrophic lateral sclerosis; neuralgia; weight regulation; obesity;
KW   anorexia nervosa; epilepsy; hemiballism; Huntington chorea; stress;
KW   Parkinson's disease; cataract; arthritis; hyperactivity;
KW   developmental disorder; rabies; infection; influenza; malaria; CJD;
KW   inflammatory bowel disease; Crohn's disease; hypertension; toxoplasmosis;
KW   asthma; autoimmunity; neuropathy; diabetes; HIV; AIDS;
KW   autonomic disorder; digestive tract disorder; nervous system disorder;
KW   neurodegeneration; Alzheimer's disease; ischemia; encephalitis;
KW   prion disease; demyelinization; multiple sclerosis; retinal degeneration;
KW   glaucoma; nystagmus; retinal detachment; ataxia; memory disorder;
KW   cognitive disorder; stiff-man syndrome; restless leg syndrome; phobia;
KW   sleep disorder; neuroinflammation; fever; taste disorder; food allergy;
KW   muscular atrophy; neurological disease; spinal motor neuron disease;
KW   aggression; paranoia; neuroendocrine disorder; Tourette syndrome;
KW   sudden infant death syndrome; cardiac infarct; insomnia; amnesia;
KW   multiple sclerosis; jet lag; sexual dysfunction; impotence; priapism;
KW   neuroprotection; enzyme.
XX
OS   Rattus sp.
XX
PN   WO200302982828-A2.
XX
PD   10-APR-2003.
XX
PF   24-SEP-2002; 2002WO-EP010707.
XX
PR   24-SEP-2001; 2001DE-01047006.
PR   25-SEP-2001; 2001DE-01047028.
XX
PA   (CHEF ) GRUENENTHAL GMBH.
XX
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PI   Weihe E, Schaefer MK;
XX
DR   WPI; 2003-354751/33.
DR   N-PSDB; ADC15485.
XX
PT   Identifying agents for treatment and diagnosis of diseases, e.g.
PT   depression or viral infections, from binding to inorganic phosphate
PT   transporters, also new agents.
XX
PS   Claim 1; Fig 1f; 129pp; German.
XX
CC   This invention describes a novel method of identifying agents for
CC   detection or treatment of specified conditions. The method comprises-
CC   incubating test compound with BNPI or DNPI (brain or differentiation-
CC   associated sodium-dependent inorganic phosphate transporter), or related
CC   proteins, nucleic acids or cells (and/or cell preparations), then
CC   measuring binding of test compound or some functional parameter altered
CC   by binding. The products of the invention have ophthalmological,
CC   auditory, neuroleptic, antimanic, antidepressant, cerebroprotective,
CC   neuroprotective, analgesic, anorectic, anticonvulsant, antiparkinsonian,
CC   vasotropic, antiemetic, antiarthritic, tranquillizer, virucide,
CC   antibacterial, procozoacide, antiinflammatory, cardiant, hypotensive,
CC   antiasthmatic, immunosuppressive, antidiabetic, antialcoholic, anti-HIV,
CC   nootropic and antiallergic activity. The method is used to identify
CC   agents for diagnosis and treatment (including gene therapy) of disorders
CC   of vision; retinitis pigmentosa; optical degeneration; hearing disorders
CC   or loss; tinnitus; Meniere's disease; schizophrenia; mania; depression;
CC   stroke; brain trauma; 'cut-through' paralysis; amyotrophic lateral
CC   sclerosis; neuralgia; weight regulation; obesity; anorexia nervosa;
CC   epilepsy; hemiballism; Huntington chorea; stress; Parkinson's disease;
CC   transient ischemic attacks; emesis (e.g. after chemotherapy); dizziness;
CC   cataract; arthritis; hyperactivity; developmental disorders; rabies;
CC   bacterial and viral infections; influenza; malaria; CJD; inflammatory
CC   bowel disease; Crohn's disease; cardio-vascular and -respiratory
CC   functional disorders; hypertension; baroafferent and chemoafferent
CC   diseases; toxoplasmosis; asthma; autoimmunity in central and peripheral
CC   nervous systems; diabetic or alcoholic neuropathy; autoimmune diabetes;
CC   HIV-neuro-AIDS; disorders of the autonomic or digestive tract nervous
CC   systems; overexcitability, particularly mediated by glutamate;
CC   neurodegeneration; Alzheimer's disease; ischemia; encephalitis (viral,
CC   bacterial, Rasmussen or HIV); prion diseases; demyelinization
CC   (particularly multiple sclerosis); retinal degeneration; glaucoma;
CC   nystagmus; retinal detachment; diseases of cerebellum (ataxia); basal
CC   ganglia, pallidum, hearing or balancing organs; auditory canal; memory,
CC   learning and cognitive disorders; stiff-man or restless leg syndromes;
CC   anxiety; phobia; sleep disorders; drug dependency; addiction or
CC   withdrawal (especially alcohol, nicotine, opiates, ecstasy or cocaine);
CC   hepatoencephalopathy, with or without alcohol intoxication;
CC   neurotoxicological diseases; spinal motor neuron diseases; muscular
CC   atrophy or dystrophy; spinal cord disease; neuroinflammation; fever;
CC   taste disorders; food allergies; Chinese restaurant syndrome; aggression;
CC   paranoia; tremors; neuroendocrine disorders; Tourette syndrome; human;
CC   cerebrovascular spasms; neuronal apoptosis or necrosis; astrocytosis;
CC   burn-out syndrome; sudden infant death syndrome; cardiac infarct;
CC   insomnia; retrograde amnesia; multiple sclerosis; jet lag; sexual
CC   dysfunction (impotence; priapism); also promotion of microglial activity,
CC   learning, cognition or memory; neuroprotection; diagnosis of neurostatic
CC   disease, and as adjuvant therapy for electrostimulation of the
CC   subthalamic nucleus in Parkinson's disease. This sequence represents the
CC   rat BNPI protein also represented in AN; U07609.
XX
SQ   Sequence 560 AA;

Query Match             98.5%;  Score 2925;  DB 7;  Length 560;
Best Local Similarity   98.2%;  Pred. No. 8e-263;
Matches  550;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGREPVTTQTRDPPVVDCTCFGLP   60
         ||||||||||||||||:||||||||||||||||||||||||||||:|||||||||||||||
Db    1 MEFRQEEFRKLAGRALGRLHRLLEKRQEGAETLELSADGREPVTTHTRDPPVVDCTCFGLP   60

Qy   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH  120
         ||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQPNWDPETVGLIH  120
```

```
RESULT 13
ABG74795
ID   ABG74795 standard; protein; 582 AA.
XX
AC   ABG74795;
XX
DT   10-JUN-2003 (first entry)
XX
DE   Human DNP1 protein.
XX
KW   BNPI; sodium-dependent inorganic phosphate cotransporter; DNPI;
KW   pain-regulation; glutamate transport mediator; musculo-skeletal
KW   pain; brain sodium-dependent inorganic phosphate cotransporter;
KW   brain inorganic phosphate cotransporter; antimigraine; chronic pain;
KW   differentiation-associated inorganic phosphate cotransporter; migraine;
KW   neuropathy; allodynia; mechanical hyperalgesia; diabetic neuropathy;
KW   visceral pain; cerebral pain; peripheral pain; inflammatory pain; human;
KW   cluster headache; trigeminal neuralgia; enzyme.
OS   Homo sapiens.
XX
PN   WO200201394-A2.
XX
PD   19-DEC-2002.
XX
PF   13-JUN-2002; 2002WO-EP006484.
XX
PR   13-JUN-2001; 2001DE-01028541.
XX
PA   (CHEP ) GRUENENTHAL GMBH.
XX
PI   Weihe E, Schaefer MK;
XX
DR   WPI; 2003-148835/14.
DR   N-PSDB; ABX13553.
XX
PT   Identifying pain-regulating compounds, useful particularly for treating
PT   chronic pain, based on interaction with specific phosphate
```

```
Db   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQPNWDPETVGLIH  120
Db  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIFSAARVHYGCVIFVRILQG  180
Qy  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIFSAARVHYGCVIFVRILQG  180
Qy  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVLQYSGWSSVFYV  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVLQYSGWSSVFYV  240
Qy  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT  300
         ||||||||||||||||||||||||||||||||||||||||||||:||||:||||||||||
Db  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPVTKFNTPWRRFFT  300
Qy  301 SMPVYAIIVANFCRSWTFYLLLISQPAYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ  360
         ||||||||||||||||||||||||:|:||||||||||||||||||||||||||||||||
Db  301 SMPVYAIIVANFCRSWTFYLLLISQDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ  360
Qy  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS  420
Qy  421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY  480
Qy  481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPS  540
         ||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db  481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDESEMEDEVEPPGAPPAPPS  540
Qy  541 YGATHSTFPQPRPPPPVRDY  560
         |||||||:||||||||||||
Db  541 YGATHSTVQPPRPPPPVRDY  560
```

RESULT 14
ADC15490

ID   ADC15490 standard; protein; 582 AA.
XX
AC   ADC15490;
XX
DT   18-DEC-2003 (first entry)
XX
DE   Human DNPI protein.
XX

PT   cotransporters.
XX
PS   Claim 1a; Fig 2b; 104pp; German.
XX
CC   This invention describes a novel method for identifying pain-regulating
CC   substances. The method comprises incubating a test substance with BNPI
CC   (brain sodium-dependent inorganic phosphate cotransporter) or DNPI
CC   (differentiation-associated sodium-dependent inorganic phosphate
CC   cotransporter then measuring either binding of the test substance to BNPI
CC   or DNPI or some functional property of the proteins that is altered by
CC   binding to the test substance. The novel pain-regulating substances have
CC   analgesic and antimigraine activity. BNPI and DNPI are mediators of
CC   glutamate transport. The products of the invention are used for treating
CC   chronic pain, particularly musculo-skeletal, neuropathic (especially
CC   allodynic pain, mechanical hyperalgesia or diabetic neuropathy);
CC   visceral, cerebral, peripheral and/or inflammatory pain, also migraine,
CC   cluster headache and trigeminal neuralgia. This sequence represents the
CC   human DNPI polypeptide encoded by the polynucleotide (deposited in
CC   AB032435) used in the method disclosed in the invention
XX
SQ   Sequence 582 AA;

Query Match   78.0%; Score 2317.5; DB 6; Length 582;
Best Local Similarity   79.4%;
Matches 429; Conservative   56; Mismatches   50; Indels   5; Gaps   2;

Qy   5 QEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLPRRYI 64
              |:|::|.:||.|||||||||:.|:..|.:|.|:||:||.|.:..||..||:|||||||||
Db   13 KEGLKNFAGKSLGQIYRVLEKKQDTGETIELTEDGKPLEVPERKAPLCDCTCFGLPRRYI 72

Qy   65 IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFF 124
              |||||||||||||||||||||||:.||||||:|||||:|:.:|:.:.||||||||:|||||
Db   73 IAIMSGLGFCISFGIRCNLGVAIVDMVNNSTIHRGGKVIKEKAKFNWDPETVGMIHGSFF 132

Qy   125 WGYIVTQLPGGFICQKFAANRVGFAIVAISTLNMLIPSAARVHYGCVIFVRILQGLVEG 184
              ||||:||:|||:|...:||||||..|:.:::||||||||||||||||||||||||||||||
Db   133 WGYIITQIPGGYIASRLAANRVFGAAILLTSTLNMLIPSAARVHYGCVIFVRILQGLVEG 192

Qy   185 VTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVAMPLAGVLVQYSGWSSVFYVYGSF 244
              |||||||||||||||||||||||||:|||||||||:|||||:::||:.||||||||||||
Db   193 VTYPACHGIWSKWAPPLERSRLATTSFCGSYAGAVIAMPLAGIILVQTYGWSSVFYVYGSF 252

Qy   245 GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPV 304
              |:.:.:.||||||||||:||:|::|||||||::|||||:|:..:.|:.|||:|||||||||
Db   253 GMWVWYMFWLLVSYESPAKHPTITDEERRYIEESIGESANLLGAMEKFKTPWRKFFTSMPV 312

Qy   305 YAIIVANFCRSWFFYLLLISQPDYFEEVFGFEISKVGLLVSALPHLVMTIIVPIIGGQIADF 364
              ||||||||||||||||||||||:||||||||||||||:|.:|:|||||||||||:||||||
Db   313 YAIIVANFCRSWFFYLLLISQPAYFEEVFGFEISKVGMLSAVPHLVMTIIVPIGGQIADF 372

Qy   365 LRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGFNV 424
              |||:::.|||.|||:||||||||||||||||||||::|||||||||||||||||||||||||
Db   373 LRSKQILSTTTVRKIMNCGGFGMEATLLLVVGYSHTRGVAISFLVLAVGFSGFAISGFNV 432

Qy   425 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVI 484
              ||||||||||||||||||||||||||||||||||||:|::||||||||||||:|||||||
Db   433 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKNKSREEWQYVFLIAALVHYGGVI 492

Qy   485 FYGVFASGEKQPWAEPEEMSEEKCGFVCHDQLAGSDDSEMEDEAEPPGAPPAPPSYGAT 544
              ||..|||||||||:|||.|||||||:.:.|:|.....:.::|.:....:...::.:.|||
Db   493 FYAIFASGEKQPWADPEETSEEKCGFIHEDEL----DEETGDITQ-NYINYGTTKSYGAT 547

KW   BNPI; DNPI;
KW   brain-associated sodium-dependent inorganic phosphate transporter;
KW   differentiation-associated inorganic phosphate transporter;
KW   ophthalmological; auditory; neuroleptic; antimanic; antidepressant;
KW   cerebroprotective; neuroprotective; analgesic; anorectic; anticonvulsant;
KW   antiparkinsonian; vasotropic; antiemetic; antiarthritic; tranquilizer;
KW   virucide; antibacterial; protozoacide; antiinflammatory; cardiant;
KW   hypotensive; antiasthmatic; immunosuppressive; antidiabetic;
KW   antialcoholic; anti-HIV; nootropic; antiallergic; gene therapy;
KW   vision disorder; retinitis pigmentosa; optical degeneration;
KW   hearing disorder; tinnitus; Meniere's disease; schizophrenia; mania;
KW   depression; stroke; brain trauma; paralysis;
KW   amyotrophic lateral sclerosis; neuralgia; weight regulation; obesity;
KW   anorexia nervosa; epilepsy; hemiballism; Huntington chorea; stress;
KW   Parkinson's disease; cataract; arthritis; hyperactivity;
KW   developmental disorder; rabies; influenza; infection; influenza; malaria; CJD;
KW   inflammatory bowel disease; Crohn's disease; hypertension; toxoplasmosis;
KW   asthma; autoimmunity; neuropathy; diabetes; HIV; AIDS;
KW   neurodegeneration; Alzheimer's disease; ischemia; encephalitis;
KW   prion disease; demyelinization; multiple sclerosis; retinal degeneration;
KW   glaucoma; nystagmus; retinal detachment; ataxia; memory disorder;
KW   cognitive disorder; stiff-man syndrome; restless leg syndrome; phobia;
KW   sleep disorder; neurological disease; spinal motor neuron disease;
KW   muscular atrophy; neuroinflammation; fever; taste disorder; food allergy;
KW   aggression; paranoia; neuroendocrine disorder; Tourette syndrome;
KW   sudden infant death syndrome; cardiac infarct; insomnia; amnesia;
KW   multiple sclerosis; jet lag; sexual dysfunction; impotence; priapism;
KW   neuroprotection; enzyme.
XX
OS   Homo sapiens.
XX
PN   WO200302S828-A2.
XX
PD   10-APR-2003.
XX
PF   24-SEP-2002; 2002WO-EP010707.
XX
PR   24-SEP-2001; 2001DE-01047006.
PR   25-SEP-2001; 2001DE-01047028.
XX
PA   (CHEF) GRUENENTHAL GMBH.
XX
PI   Weihe E, Schaefer MK;
XX
DR   N-PSDB; ADC15489.
DR   WPI; 2003-354751/33.
XX
PS   Claim 1; Fig 2b; 129pp; German.
XX
PT   Identifying agents for treatment and diagnosis of diseases, e.g.
PT   depression or viral infections, from binding to inorganic phosphate
PT   transporters, also new agents.
XX
CC   This invention describes a novel method of identifying agents for
CC   detection or treatment of specified conditions. The method comprises
CC   incubating test compound with BNPI or DNPI (brain or differentiation-
CC   associated sodium-dependent inorganic phosphate transporter), or related
CC   proteins, nucleic acids or cells (and/or cell preparations), then
CC   measuring binding of test compound or some functional parameter altered
CC   by binding. The products of the invention have ophthalmological,
CC   auditory, neuroleptic, antimanic, antidepressant, cerebroprotective,
CC   neuroprotective, analgesic, anorectic, anticonvulsant, antiparkinsonian,
CC   vasotropic, antiemetic, antiarthritic, tranquillizer, virucide,
CC   antibacterial, protozoacide, antiinflammatory, cardiant, hypotensive,
CC   antiasthmatic, immunosuppressive, antidiabetic, antialcoholic, anti-HIV,
CC   nootropic and antiallergic activity. The method is used to identify
CC   agents for diagnosis and treatment (including gene therapy) of disorders
CC   of vision; retinitis pigmentosa; optical degeneration; hearing disorders
CC   or loss; tinnitus; Meniere's disease; schizophrenia; mania; depression;
CC   stroke; brain trauma; 'cut-through' paralysis; amyotrophic lateral
CC   sclerosis; neuralgia; weight regulation; obesity; anorexia nervosa;
CC   epilepsy; hemiballism; Huntington chorea; stress; Parkinson's disease;

```
CC   transient ischemic attacks; emesis (e.g. after chemotherapy); dizziness;
CC   cataract; arthritis; hyperactivity; developmental disorders; rabies;
CC   bacterial and viral infections; influenza; malaria; CJD; inflammatory
CC   bowel disease; Crohn's disease; cardio-vascular and -respiratory
CC   functional disorders; hypertension; baroafferent and chemoafferent
CC   diseases; toxoplasmosis; asthma; autoimmunity in central and peripheral
CC   nervous systems; diabetic or alcoholic neuropathy; autoimmune diabetes;
CC   HIV-neuro-AIDS; disorders of the autonomic or digestive tract nervous
CC   systems; overexcitability, particularly mediated by glutamate;
CC   neurodegeneration; Alzheimer's disease; ischemia; encephalitis (viral,
CC   bacterial, Ramussen or HIV); prion diseases; demyelinization
CC   (particularly multiple sclerosis), retinal degeneration; glaucoma;
CC   nystagmus; retinal detachment; diseases of cerebellum (ataxia), basal
CC   ganglia, pallidum, hearing or balancing organs, auditory canal; memory,
CC   learning and cognitive disorders; stiff-man or restless leg syndromes;
CC   anxiety; phobia; sleep disorders; drug dependency, addiction or
CC   withdrawal (especially alcohol, nicotine, opiates, ecstasy or cocaine);
CC   hepatoencephalopathy, with or without alcohol intoxication;
CC   neurotoxicological diseases; spinal motor neuron diseases; muscular
CC   atrophy or dystrophy; spinal cord disease; neuroinflammation; fever;
CC   taste disorders; food allergies; Chinese restaurant syndrome; aggression;
CC   paranoia; tremors; neuroendocrine disorders; Tourette syndrome;
CC   cerebrovascular spasms; neuronal apoptosis or necrosis; astrocytosis;
CC   burn-out syndrome; sudden infant death syndrome; cardiac infarct;
CC   insomnia; retrograde amnesia; multiple sclerosis; jet lag; sexual
CC   dysfunction (impotence; priapism) also promotion of microglial activity,
CC   learning, cognition or memory; neuroprotection; diagnosis of neurostatic
CC   disease, and as adjuvant therapy for electrostimulation of the
CC   subthalamic nucleus in Parkinson's disease. This sequence represents the
CC   human DNPI protein described in the disclosure of the invention.
XX
SQ   Sequence 582 AA;

Qy   Query Match             429; 
Best Local Similarity   78.0%; 
Matches    429; Conservative  79.4%; Pred. No. 2.7e-206;  
                        Score 2317.5; DB 7; Length 582;
                        Mismatches  50; Indels   5; Gaps   2;

Qy      5 QEEFRKLAGRALGKLHRLLEKRQEGAETELSADGRPVTIQTRDPPVVDCTCFGLPRRYI 64
          :   |||||::|:|||:|::::|||||||||||||:   |::||||||:|||||||||||
Db     13 KEGLKNFAGKSLGQIYRVLEKKQDTCGETIELTEDGKPLEVPERKAPLCDCTCFGLPRRYI 72

Qy     65 IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGHVVVQKAQFSWDPETVGLIHGSFF 124
          ||||||||||||||||||||||||.||||||.|||.||:|||||.||||||.|||||||
Db     73 IAIMSGLGFCISFGIRCNLGVAIVDMVNNSTIHRGGKVIKEKAKFNWDPETVGMIHGSFF 132

Qy    125 WGYIVTQIPGGFICQKFAAARVFGFRAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEG 184
          ||||:||||||:|.::.|||.|||:||:::|||||||||||||||||||||||||||||||
Db    133 WGYIITQIPGGYIASRLAAANRVFGAAILLTSTLNMLIPSAARVHYGCVIFVRILQGLVEG 192

Qy    185 VTYPACHGIWSKWAPPLERSRLATTAPCGSYAGAVVAMPLAGVLVQYSGWSSVFYVYGSF 244
          |||||||||||||||||||||||||:.|||||||||:||||||:||||:|||||||||||
Db    193 VTYPACHGIWSKWAPPLERSRLATTSFCGSYAGAVIAMPLAGIILVQYTGWSSVFYVYGSF 252

Qy    245 GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGRESAKLMNPLTKFSTPWRRFFTSMPV 304
          |:.||.||||||||||:.|.:..||||||||:|||||||:|:..:.||.|||||||||||||
Db    253 GMVWYWFWLLVSYESPAKHPITTDEERRYIEESIGRESANLLGAMEKFKTPWRKFFTSMPV 312

Qy    305 YAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKYGLVSALPHLVWTILVPIGGQIADF 364
          |||||||||||||||||||||||:||||||||||||||:||.|||||:|:||||||:|||
Db    313 YAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKYGMLSAVPHLVMTIIVPIGGQTADF 372

Qy    365 LRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGVSHSRGVAISFLVLAVGFSGFAISGFNV 424
          |||.:|:|||.|||:|||||||||||||:|||||:|.|||||||:|||||||||||||||
Db    373 LRSKQILSTTTVRKIMNCGGFGMEATLLIVVGVSYSHRGVAISFVLAVGFSGFAISGFNV 432

Qy    425 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHTKREWQYVFLIASLVHYGGVI 484
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Db    433 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKNKSREEWQYVFLIAALVHVGGVI 492

Qy    485 FYGVPASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDDEAEPGAPPAPPPSYGAT 544
          ||.:.|||||||||:|||:|||||||:..|:|         ::::. :    |:||||||
Db    493 FYAIFASGEKQPWADPEETSEEKCGFIHEDEL-----DEETGDITQ-NYINYGTTKSYGAT 547
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Human VGLUT2 protein sequence.

```
XX
KW   antidiabetic; antilipemic; antiarteriosclerotic; nootropic;
KW   neuroprotective; anabolic; antiinflammatory; immunosuppressive;
KW   cytostatic; antiallergic; antiasthmatic; cerebroprotective;
KW   antiallergic; dermatological; cardiant; antiParkinsonian; neuroleptic;
KW   glucose transporter; potassium ion channel protein; diabetes;
KW   hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;
KW   colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;
KW   sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;
KW   meningitis; hepatitis; myocarditis; asthma; immune disorder;
KW   multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;
KW   allergy; hay fever; allergic rhinitis; anaphylactic shock;
KW   atopic dermatitis; circulatory disorder; heart failure; cancer;
KW   Alzheimer's disease; Parkinson's disease; schizophrenia;
KW   hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.
XX
OS   Homo sapiens.
XX
PN   WO2003054190-A1.
XX
PD   03-JUL-2003.
XX
PF   19-DEC-2002; 2002WO-JP013290.
XX
PR   21-DEC-2001; 2001JP-00389351.
PR   25-DEC-2001; 2001JP-00392577.
PR   26-DEC-2001; 2001JP-00394947.
PR   26-DEC-2001; 2001JP-00395467.
PR   06-FEB-2002; 2002JP-00030010.
PR   08-FEB-2002; 2002JP-00033095.
PR   06-JUN-2002; 2002JP-00165336.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Nakanishi A, Sagiya Y, Uno Y;
XX
DR   WPI; 2003-541817/51.
XX
PT   Glucose transporter TCH099, vesicular glutamate transporter TCH177 and
PT   potassium channel protein TCH136 and DNA encoding them for diagnosis,
PT   treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and
PT   digestive disorders.
XX
PS   Disclosure; Fig 3; 221pp; Japanese.
```

The invention relates to a novel glucose transporter TCH099, vesicular
glutamate transporter TCH177 and voltage-dependent potassium ion channel
protein TCH136. The sequences are useful in the treatment, prevention and
diagnosis of a broad range of diseases including diabetes, hyperlipemia,
arteriosclerosis, digestive disorders (such as Crohn's disease, colitis,
gastritis, ileitis and rectal inflammation), inflammatory diseases,
sepsis, prostatic hypertrophy, reproductive disorders, pneumonia,
meningitis, hepatitis, myocarditis, asthma, immune disorders (such as
multiple sclerosis, rheumatoid arthritis, Sjogren's disease and lupus),
allergies (such as hay fever, allergic rhinitis, anaphylactic shock and
atopic dermatitis), circulatory disorders (such as heart failure), cancer
(such as cancer of the lung, kidney, liver, ovary, prostate, stomach,
pancreas, bladder, breast, fallopian tubes or colon), central nervous
system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and
secretory disorders (such hyperprolactinemia and Cushing's disease). This
sequence represents the protein which was used for comparison with the novel
human vesicular glutamate transporter TCH177.

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SQ   Sequence 582 AA;

     Query Match          78.0%;   Score 2317.5;  DB 7;  Length 582;
     Best Local Similarity   79.4%;   Pred. No. 2.7e-206;
     Matches  429;  Conservative  56;  Mismatches  50;  Indels  5;  Gaps  2;

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          : |   || ||| |   ::| ||:|||:  |  | :|    :| |||::| |||||||||
Db     13 KEGLKNFAGKSLGQIYRVLEKKQDTGEITELTEDGKPLEVPERKAPLCDCTCFGLPRRYI   72

Qy     65 IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFF  124
          |||||||||||||||||||||||||| |:|:|:|||||:||:|||| |||:|||||||||
Db     73 IAIMSGLGFCISFGIRCNLGVAIVDMVNNSTIHRGGKVIKEKAKFNWDPETVGMIHGSFF  132

Qy    125 WGYIVTQIPGGFICQKFAANRVPGFAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEG  184
          ||||:||||||:||:||:| |:  :||:|||||||||||||||||||||||||||||||||
Db    133 WGYIITQIPGGYIASRLAANRVFGAAILLTSTLNMLIPSAARVHYGCVIFVRILQGLVEG  192

Qy    185 VTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVPYVYGSF  244
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Db    193 VTYPACHGIWSKWAPPLERSRLATTSFCGSYAGAVIAMPLAGIILVQYTGWSSVPYVYGSF  252

Qy    245 GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPV  304
          || :| |  ||||| || |  |:||||||||| | ||| |:||:|||:| |||:||||||
Db    253 GMVWYMFWLLVSYESPAKHPTITDEERYIEESIGESANLLGAMEKFKTPWRKPFTSMPV  312

Qy    305 YAIIVANPCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADF  364
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Db    313 YAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGMLSAVPHLVMTIIVPIGGQIADF  372

Qy    365 LRSRRIMSTTNVRKLMNCGFGNMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGFNV  424
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Db    373 LRSKQILSTTTVRKIMNCGFGNMEATLLLVVGYSHTRGVAISFLVLAVGFSGFAISGFNV  432

Qy    425 NHLDIAPRYASILMGISNGVGTLLSGMVCPIIVGAMTKIKTREEWQYVFLIASLVHYGGVI  484
          ||||||||||||||||||||||||||||||||||: |:|::|||||||::|| ||||||:
Db    433 NHLDIAPRYASILMGISNGVGTLLSGMVCPIIVGAMTKNKSREEWQYVFLIAALVHYGGVI  492

Qy    485 FYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPSYGAT  544
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Db    493 FYAIFASGEKQPWADPEETSEEKCGFIHEDEL----DEETGDITQ-NYINYGTTKSYGAT  547
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 2, 2005, 11:25:48 ; Search time 479 Seconds
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         1365.519 Million cell updates/sec

Title: US-10-734-731-4
Perfect score: 2970
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Scoring table: BLOSUM62
      Gapop 10.0 , Gapext 0.5
Searched: 6959266 seqs, 116006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
      Maximum Match 100%
      Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2970	100.0	560	8	US-08-430-733-1	Sequence 5, Appli
2	2970	100.0	560	33	US-10-734-731-4	Sequence 4, Appli
3	2970	100.0	560	34	US-10-807-500-4	Sequence 5, Appli
4	2967	99.9	560	1	PCT-US98-02875-5	Sequence 5, Appli
5	2967	99.9	560	1	PCT-US98-02875A-5	GENERAL INFORMA
6	2967	99.9	560	17	US-09-380-164-5	Sequence 5, Appli
7	2967	99.9	560	29	US-10-314-790-5	Sequence 2, Appli
8	2967	99.9	560	37	US-60-039-462-5	Sequence 5, Appli
9	2962	99.7	560	27	US-10-170-205E-18690	Sequence 18690, A
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11	2962	99.7	560	1	PCT-US98-2875-5	Sequence 5598, Ap
12	2962	99.7	560	29	US-10-756-149-5598	Sequence 2, Appli
13	2962	99.7	560	37	US-10-807-500-2	Sequence 12892, A
14	2962	99.7	560	37	US-60-452-680-12892	Sequence 8103, Ap
15	2962	99.7	560	37	US-60-453-050-8103	Sequence 8103, Ap
16	2962	99.7	560	37	US-60-453-135-8103	Sequence 8103, A
17	2962	99.7	567	28	US-10-220-366A-27762	Sequence 27762, A
18	2962	99.7	567	35	US-10-940-774-11354	Sequence 11354, A
19	2929	98.6	560	33	US-10-734-731-8	Sequence 8, Appli
20	2929	98.6	560	34	US-10-807-500-8	Sequence 8, Appli
21	2925	98.5	560	25	US-09-965-522-4	Sequence 4, Appli
22	2925	98.5	560	25	US-09-991-212-4	Sequence 4, Appli
23	2925	98.5	560	25	US-09-991-212A-4	Sequence 4, Appli
24	2925	98.5	560	33	US-10-734-731-6	Sequence 6, Appli
25	2925	98.5	560	34	US-10-807-500-6	Sequence 6, Appli
26	2925	98.5	560	34	US-10-877-818-4	Sequence 4, Appli
27	2317.5	98.0	582	27	US-10-170-205E-23413	Sequence 23413, A
28	2317.5	78.0	582	33	US-10-734-731-10	Sequence 10, Appli
29	2317.5	78.0	582	34	US-10-807-500-10	Sequence 10, Appli
30	2313.5	77.9	578	29	US-10-389-967-4	Sequence 4, Appli
31	2313.5	77.9	582	28	US-10-205-331-7	Sequence 7, Appli
32	2313.5	77.9	582	33	US-10-734-731-12	Sequence 12, Appli
33	2313.5	77.9	582	33	US-10-734-731-14	Sequence 14, Appl
34	2313.5	77.9	582	34	US-10-807-500-12	Sequence 12, Appl
35	2313.5	77.9	582	34	US-10-807-500-14	Sequence 14, Appl
36	2307.5	77.7	582	27	PCT-US01-04098A-1935	Sequence 1935, Ap
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40	2185	73.6	589	29	US-10-389-967-2	Sequence 2, Appli
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42	2185	73.6	589	33	US-10-777-288A-3527	Sequence 3527, Ap
43	2154.5	72.5	601	30	US-10-499-731-46	Sequence 46, Appl
44	2138.5	72.0	566	1	PCT-US02-35464-300	Sequence 300, App
45	2138.5	72.0	566	28	US-10-287-226-300	Sequence 300, App

ALIGNMENTS

RESULT 1
US-08-430-033-2
; Sequence 2, Application US/08430033
; GENERAL INFORMATION:
; APPLICANT: Ni, Binhui
; APPLICANT: Paul, Steven M.
; TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
; TITLE OF INVENTION: PHOSPHATE COTRANSPORTER AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,033
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-430-033-2

Query Match   100.0%;   Score 2970;   DB 8;   Length 560;
Best Local Similarity   100.0%;   Pred. No. 1.8e-272;
Matches 560; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVAVAMPLAGVLVQYSGWSSSVFYV 240
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Qy    301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
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Qy    361 IADFLRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
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Db    541 YGATHSTFQPPRPPPPVRDY 560
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RESULT 2
Sequence 4, Application US/10734731
; GENERAL INFORMATION:
; APPLICANT: WEIHE, EBERHARD
; APPLICANT: SCHAFER, MARTIN
; TITLE OF INVENTION: SCREENING METHOD USING BNPI AND DNPI

; FILE REFERENCE: 029310.5299US
; CURRENT APPLICATION NUMBER: US/10/734,731
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: PCT/EP02/06484
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: DE 101 28 541.8
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 3.2
; ORGANISM: Homo sapiens
; SEQ ID NO 4
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-734-731-4

Query Match   100.0%;   Score 2970;   DB 33;   Length 560;
Best Local Similarity   100.0%;   Pred. No. 1.8e-272;
Matches 560; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy     61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVVQKAQFSWDPETVGLIH 120
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Qy    121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
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Qy    181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVAVAMPLAGVLVQYSGWSSSVFYV 240
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Qy    241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
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Qy    301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
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Db    301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy    361 IADFLRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
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Db    361 IADFLRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy    421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
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Db    421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy    481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540

Qy    541 YGATHSTFQPPRPPPPVRDY 560
          ||||||||||||||||||||
Db    541 YGATHSTFQPPRPPPPVRDY 560
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RESULT 3
US-10-807-500-4
; Sequence 4, Application US/10807500
; GENERAL INFORMATION:
; APPLICANT: WEIHE, EBERHARD
; APPLICANT: SCHAFER, MARTIN
; TITLE OF INVENTION: SCREENING PROCESS FOR VARIOUS INDICATIONS USING BNPI AND/OR DNPI
; FILE REFERENCE: 029310.5335US
; CURRENT APPLICATION NUMBER: US/10/807,500
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: PCT/EP02/10707
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: DE 101 47 006.1

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PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: DE 101 47 028.2
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 4
LENGTH: 560
TYPE: PRT
ORGANISM: Homo sapiens
US-10-807-500-4
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Query Match   100.0%;   Score 2970;   DB 34;   Length 560;
Best Local Similarity   100.0%;   Pred. No. 1.8e-272;
Matches 560;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGEAETLELSADGRPVTTQTRDPPVVDCTCFGLP  60
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Db    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGEAETLELSADGRPVTTQTRDPPVVDCTCFGLP  60

Qy   61 RRYIIAIMSGLGFCISPGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RRYIIAIMSGLGFCISPGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120

Qy  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLITKFSTPWRRFT 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLITKFSTPWRRFT 300

Qy  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy  421 GFNVNHLDIAPRYASILMGISNGVGTLLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GFNVNHLDIAPRYASILMGISNGVGTLLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy  481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540

Qy  541 YGATHSTFQPPRPPPPVRDY 560
        ||||||||||||||||||||
Db  541 YGATHSTFQPPRPPPPVRDY 560
```

RESULT 4
PCT-US98-02875-5
Sequence 5, Application PC/TUS9802875

GENERAL INFORMATION:
  APPLICANT: EMORY UNIVERSITY
  APPLICANT: Gunn, Robert B.
  APPLICANT: Timmer, Richard T.
  TITLE OF INVENTION: SODIUM-PHOSPHATE COTRANSPORTER IN
  TITLE OF INVENTION: LITHIUM THERAPY FOR THE TREATMENT OF MENTAL ILLNESS
  NUMBER OF SEQUENCES: 12
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Kilpatrick Stockton LLP
  STREET: Suite 2800, 1100 Peachtree Street NE
  CITY: Atlanta
  STATE: GA
  COUNTRY: USA
  ZIP: 30309-4530

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COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: PCT/US98/02875
  FILING DATE: 11-FEB-1998
  CLASSIFICATION:
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 60/039,462
  FILING DATE: 7-FEB-1997
ATTORNEY/AGENT INFORMATION:
  NAME: Meredith, Roy D.
  REGISTRATION NUMBER: 30,777
  REFERENCE/DOCKET NUMBER: EMU153PCT
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (404) 815-6500
  TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
  LENGTH: 560 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: peptide
  HYPOTHETICAL: NO
  ANTI-SENSE: NO
  FRAGMENT TYPE: N-terminal
FEATURE:
  NAME/KEY: hBNPI
  LOCATION: 1..560
PUBLICATION INFORMATION:
  DOCUMENT NUMBER: Ni, B., et al.,
  DOCUMENT NUMBER: J. Neurochem., 66:2227 (1996)
PCT-US98-02875-5
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Query Match   99.9%;   Score 2967;   DB 1;   Length 560;
Best Local Similarity   99.8%;   Pred. No. 3.5e-272;
Matches 559;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGEAETLELSADGRPVTTQTRDPPVVDCTCFGLP  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGEAETLELSADGRPVTTQTRDPPVVDCTCFGLP  60

Qy   61 RRYIIAIMSGLGFCISPGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RRYIIAIMSGLGFCISPGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120

Qy  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLITKFSTPWRRFT 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLITKFSTPWRRFT 300

Qy  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy  421 GFNVNHLDIAPRYASILMGISNGVGTLLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GFNVNHLDIAPRYASILMGISNGVGTLLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
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Qy 481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPS 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPS 540

Qy 541 YGATHSTFQPPRPPPPVRDY 560
         ||||||||||||||||||||
Db 541 YGATHSTFQPPRPPPPVRDY 560

RESULT 5
PCT-US98-02875A-5
Sequence 5, Application PC/TUS980287SA
GENERAL INFORMATION:
; APPLICANT: EMORY UNIVERSITY
; APPLICANT: Gunn, Robert B.
; APPLICANT: Timmer, Richard T.
; TITLE OF INVENTION: SODIUM-PHOSPHATE COTRANSPORTER IN
; TITLE OF INVENTION: LITHIUM THERAPY FOR THE TREATMENT OF MENTAL ILLNESS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick Stockton LLP
; STREET: Suite 2800, 1100 Peachtree Street NE
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/02875A
; FILING DATE: 11-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,462
; FILING DATE: 27-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Meredith, Roy D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: EMU153PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 815-6500
; TELEFAX: (404) 815-6555
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: hBNPI
; LOCATION: 1..560
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: Ni, B., et al.,
; DOCUMENT NUMBER: J. Neurochem., 66:2227 (1996)

Query Match   99.9%; Score 2967; DB 1; Length 560;
Best Local Similarity 99.8%; Pred. No. 3.5e-272;
Matches 559; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1   MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
        ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db 1   MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETVELSADGRPVTTQTRDPPVVDCTCFGLP 60

Qy 61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGHVVVQKAQFSWDPETVGLIH 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGHVVVQKAQFSWDPETVGLIH 120

RESULT 6
US-09-380-164-5
Sequence 5, Application US/09380164
GENERAL INFORMATION:
; APPLICANT: EMORY UNIVERSITY
; APPLICANT: Gunn, Robert B.
; APPLICANT: Timmer, Richard T.
; TITLE OF INVENTION: SODIUM-PHOSPHATE COTRANSPORTER IN
; TITLE OF INVENTION: LITHIUM THERAPY FOR THE TREATMENT OF MENTAL ILLNESS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick Stockton LLP
; STREET: Suite 2800, 1100 Peachtree Street NE
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/380,164
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/02875
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meredith, Roy D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: EMU153PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 815-6500
; TELEFAX: (404) 815-6555
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:

Qy 121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVAIVTSLLNMLIPSAARVHYGCVIFVRILQG 180
         |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db 121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVAITSTLLNMLIPSAARVHYGCVIFVRILQG 180

Qy 181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLIVQYSGWSSVFYV 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLIVQYSGWSSVFYV 240

Qy 241 YGSFGIFWLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 YGSFGIFWLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300

Qy 301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy 361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy 421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy 481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPS 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPS 540

Qy 541 YGATHSTFQPPRPPPPVRDY 560
         ||||||||||||||||||||
Db 541 YGATHSTFQPPRPPPPVRDY 560

LENGTH: 560 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: hNPI
LOCATION: 1..560
PUBLICATION INFORMATION:
DOCUMENT NUMBER: Ni, B., et al.,
PUBLICATION NUMBER: J. Neurochem., 66:2227 (1996)

US-09-380-164-5
DOCUMENT NUMBER: US-09-380-164-5

Query Match
Best Local Similarity 99.9%; Score 2967; DB 17; Length 560;
Matches 559; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Pred. No. 3.5e-272;

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Qy    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP   60
        ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETVELSADGRPVTTQTRDPPVVDCTCFGLP   60

Qy   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH  120

Qy  121 GSFFWGVIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRLLQG  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GSFFWGVIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRLLQG  180

Qy  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV  240

Qy  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT  300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT  300

Qy  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ  360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ  360

Qy  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS  420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS  420

Qy  421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY  480

Qy  481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS  540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS  540

Qy  541 YGATHSTFQPRPPPPPVRDY  560
        ||||||||||||||||||||
Db  541 YGATHSTFQPRPPPPPVRDY  560
```

CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-4530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/314,790
FILING DATE: 09-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/380,164
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/US98/02875
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Meredith, Roy D.
REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: EMU153PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6500
TELEFAX: (404) 815-6555
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-314-790-5

Query Match
Best Local Similarity 99.9%; Score 2967; DB 29; Length 560;
Matches 559; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Pred. No. 3.5e-272;

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Qy    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP   60
        ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETVELSADGRPVTTQTRDPPVVDCTCFGLP   60

Qy   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH  120

Qy  121 GSFFWGVIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRLLQG  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GSFFWGVIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRLLQG  180

Qy  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV  240

Qy  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT  300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT  300

Qy  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ  360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ  360

Qy  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS  420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS  420

Qy  421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY  480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY  480

Qy  481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS  540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS  540

Qy  541 YGATHSTFQPRPPPPPVRDY  560
        ||||||||||||||||||||
Db  541 YGATHSTFQPRPPPPPVRDY  560
```

RESULT 7
US-10-314-790-5
GENERAL INFORMATION:
APPLICANT: EMORY UNIVERSITY
Gunn, Robert B.
Timmer, Richard T.
TITLE OF INVENTION: SODIUM-PHOSPHATE COTRANSPORTER IN
LITHIUM THERAPY FOR THE TREATMENT OF MENTAL ILLNESS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick Stockton LLP
STREET: 1100 Peachtree Street NE
Suite 2800,

RESULT 8
US-60-039-462-5
Sequence 5, Application US/60039462
; GENERAL INFORMATION:
; APPLICANT: Gunn, Robert B.
; APPLICANT: Timmer, Richard T.
; TITLE OF INVENTION: SODIUM-PHOSPHATE COTRANSPORTER IN
; TITLE OF INVENTION: LITHIUM THERAPY FOR THE TREATMENT OF MENTAL ILLNESS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick Stockton LLP
; STREET: Suite 2800, 1100 Peachtree Street NE
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/039,462
; FILING DATE: 27-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meredith, Roy D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: E269/99809-EMU153
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 815-6500
; TELEFAX: (404) 815-6555
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
; ANTI-SENSE: NO
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: hBNPI
; LOCATION:
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: Ni, B., et al., 66:2227 (1996)
; DOCUMENT NUMBER: J. Neurochem.,
US-60-039-462-5

Query Match   99.9%; Score 2967; DB 37; Length 560;
Best Local Similarity 99.8%; Pred. No. 3.5e-272;
Matches 559; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60

Qy   61 RRYIIAIMSGLGFCISFGTRCNLGVAIVSMVNNSTTHRGGHVVVQKAQPSWDPETVGLIH 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RRYIIAIMSGLGFCISFGTRCNLGVAIVSMVNNSTTHRGGHVVVQKAQPSWDPETVGLIH 120

Qy  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSSVFYV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSSVFYV 240

Qy  241 YGSFGIWWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 YGSFGIWWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300

Qy  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGSGFAIS 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGSGFAIS 420

Qy  421 GFNNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GFNNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy  481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540

Qy  541 YGATHSTFQPPRPPPPVRDY 560
        ||||||||||||||||||||
Db  541 YGATHSTFQPPRPPPPVRDY 560
```

RESULT 9
US-10-170-205E-18690
Sequence 18690, Application US/10170205E
; GENERAL INFORMATION:
; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
; FILE REFERENCE: CL001381
; CURRENT APPLICATION NUMBER: US/10/170,205E
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 18690
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-18690

Query Match   99.7%; Score 2962; DB 27; Length 560;
Best Local Similarity 99.8%; Pred. No. 1e-271;
Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60

Qy   61 RRYIIAIMSGLGFCISFGTRCNLGVAIVSMVNNSTTHRGGHVVVQKAQPSWDPETVGLIH 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RRYIIAIMSGLGFCISFGTRCNLGVAIVSMVNNSTTHRGGHVVVQKAQPSWDPETVGLIH 120

Qy  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSSVFYV 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSSVFYV 240

Qy  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300

Qy  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGSGFAIS 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGSGFAIS 420

Qy  421 GFNNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 GFNNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
```

RESULT 10
US-10-734-731-2
Sequence 2, Application US/10734731
; GENERAL INFORMATION:
; APPLICANT: WEIHE, EBERHARD
; APPLICANT: SCHAFER, MARTIN
; TITLE OF INVENTION: SCREENING METHOD USING BNPI AND DNPI
; FILE REFERENCE: 029310.5299US
; CURRENT APPLICATION NUMBER: US/10/734,731
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: PCT/EP02/06484
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: DE 101 28 541.8
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 2
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-734-731-2

Query Match   99.7%; Score 2962; DB 33; Length 560;
Best Local Similarity   99.8%; Pred. No. 1e-271;
Matches 559; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy         1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60

Qy        61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120

Qy       121 GSFFWGYIVTQIPGGFICQKFAANRVGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GSFFWGYIVTQIPGGFICQKFAANRVGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy       181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy       241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300

Qy       301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy       361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy       421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy       481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540

Qy       541 YGATHSTFQPPRPPPPVVRDY 560
             |||||||||||||||||||||
Db       541 YGATHSTFQPPRPPPPVVRDY 560
```

RESULT 11
US-10-756-149-5598
Sequence 5598, Application US/10756149
; GENERAL INFORMATION:
; APPLICANT: Zlotnik, Albert
; APPLICANT: Aziz, Natasha
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5598
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-756-149-5598

Query Match   99.7%; Score 2962; DB 33; Length 560;
Best Local Similarity   99.8%; Pred. No. 1e-271;
Matches 559; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy         1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60

Qy        61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120

Qy       121 GSFFWGYIVTQIPGGFICQKFAANRVGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GSFFWGYIVTQIPGGFICQKFAANRVGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy       181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy       241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300

Qy       301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy       361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy       421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy       481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540

Qy       541 YGATHSTFQPPRPPPPVVRDY 560
             |||||||||||||||||||||
Db       541 YGATHSTFQPPRPPPPVVRDY 560
```

RESULT 12
US-10-807-500-2
; Sequence 2, Application US/10807500

GENERAL INFORMATION:
; APPLICANT: WEIHE, EBERHARD
; APPLICANT: SCHAFER, MARTIN
; TITLE OF INVENTION: SCREENING PROCESS FOR VARIOUS INDICATIONS USING BNPI AND/OR DNPI
; FILE REFERENCE: 02910.5335US
; CURRENT APPLICATION NUMBER: US/10/807,500
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: PCT/EP02/10707
; PRIOR APPLICATION FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: DE 101 47 006.1
; PRIOR APPLICATION FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: DE 101 47 028.2
; PRIOR APPLICATION FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 3.2

; SEQ ID NO 2
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-500-2

Query Match   99.7%; Score 2962; DB 34; Length 560;
Best Local Similarity   99.8%; Pred. No. 1e-271;
Matches   559; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETTLELSADGRPVTTQTRDPPVVDCTCFGLP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETTLELSADGRPVTTQTRDPPVVDCTCFGLP 60

Qy   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120

Qy   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300

Qy   301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy   361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy   421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540

Qy   541 YGATHSTFQPPRPPPVRDY 560
           ||||||||||||||||||
Db   541 YGATHSTFQPPRPPPVRDY 560

RESULT 13
US-60-452-680-12892
; Sequence 12892, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 12892
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-12892

Query Match   99.7%; Score 2962; DB 37; Length 560;
Best Local Similarity   99.8%; Pred. No. 1e-271;
Matches   559; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETTLELSADGRPVTTQTRDPPVVDCTCFGLP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETTLELSADGRPVTTQTRDPPVVDCTCFGLP 60

Qy   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120

Qy   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300

Qy   301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy   361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy   421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540

Qy   541 YGATHSTFQPPRPPPVRDY 560
           ||||||||||||||||||
Db   541 YGATHSTFQPPRPPPVRDY 560

RESULT 14
US-60-453-050-8103
; Sequence 8103, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: CL001457
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US/60/453,050
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8103
; LENGTH: 560
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-60-453-050-8103

Query Match         99.7%;      Score 2962;   DB 37;   Length 560;
Best Local Similarity   99.8%;   Pred. No. 1e-271;
Matches 559;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Qy     1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
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Db     1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60

Qy    61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
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Db   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
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Db   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
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Db   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300

Qy   301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
         ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   301 SMPVYAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy   361 IADFLRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 IADFLRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy   421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
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Db   421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
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Db   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540

Qy   541 YGATHSTFQPPRPPPPVRDY 560
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Db   541 YGATHSTFQPPRPPPPVRDY 560


RESULT 15
US-60-453-135-8103
; Sequence 8103, Application US/60453135
; GENERAL INFORMATION:
;   APPLICANT: CARGILL, Michele
;   APPLICANT: IAKOUBOVA, Olga
;   TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;   TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: CL001456
;   CURRENT APPLICATION NUMBER: US/60/453,135
;   CURRENT FILING DATE: 2003-03-10
;   NUMBER OF SEQ ID NOS: 82762
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8103
;   LENGTH: 560
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-60-453-135-8103

Query Match         99.7%;      Score 2962;   DB 37;   Length 560;
Best Local Similarity   99.8%;   Pred. No. 1e-271;
Matches 559;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Qy     1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60

Qy    61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120

Qy   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
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Db   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300

Qy   301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
         ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   301 SMPVYAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy   361 IADFLRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 IADFLRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy   421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
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Qy   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
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Db   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540

Qy   541 YGATHSTFQPPRPPPPVRDY 560
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Db   541 YGATHSTFQPPRPPPPVRDY 560


Search completed: June 2, 2005, 11:41:01
Job time : 481 secs
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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - protein search, using sw model

Run on:      June 2, 2005, 11:31:49 ; Search time 140 seconds
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                          1382.720 Million cell updates/sec

Title:          US-10-734-731-4
Perfect score:  2970
Sequence:       1 MEFRQEEFRKLAGRALGKLH.........YGATHSTFQPRPPPPVRDY 560

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       1465611 seqs, 34679903 residues

Total number of hits satisfying chosen parameters:   1465611

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2967	99.9	560	15	US-10-314-790-5	Sequence 4, Appli
2	2925	98.5	560	9	US-09-991-212A-4	Sequence 5, Appli
3	2925	98.5	560	10	US-09-915-181A-5	Sequence 4, Appli
4	2925	98.5	560	17	US-10-877-818-4	Sequence 4, Appli
5	2925	98.5	578	9	US-09-740-041-4	Sequence 4, Appli
6	2313.5	77.9	578	14	US-10-389-967-4	Sequence 4, Appli
7	2313.5	77.9	582	9	US-09-915-181A-4	Sequence 7, Appli
8	2313.5	77.9	582	15	US-10-205-331-7	Sequence 2, Appli
9	2313.5	77.9	589	9	US-09-915-181A-4	Sequence 2, Appli
10	2185	73.6	589	14	US-10-389-967-2	Sequence 2, Appli
11	2185	73.6	850	9	US-09-915-181A-3	Sequence 300, App
12	2174.5	73.2	566	15	US-10-287-226-300	Sequence 300, App
13	2138.5	72.0	566	15	US-10-287-226-300	
14	1297	43.7	576	14	US-10-014-079A-1	Sequence 1, Appli
15	1297	43.7	576	15	US-10-369-493-5823	Sequence 5823, Ap
16	1294	43.6	563	9	US-09-915-181A-6	Sequence 6, Appli
17	1186	39.9	264	15	US-10-108-260A-3281	Sequence 3281, Ap
18	1025.5	34.5	204	15	US-10-104-047-2253	Sequence 2253, Ap
19	971	32.7	573	15	US-10-369-493-5871	Sequence 5871, Ap
20	971	32.7	573	15	US-10-369-493-5872	Sequence 5872, Ap
21	950	32.0	544	15	US-10-369-493-5873	Sequence 5873, Ap
22	940	31.6	495	9	US-09-915-181A-7	Sequence 7, Appli
23	940	31.6	495	16	US-10-755-889-588	Sequence 588, App
24	940	31.6	495	16	US-10-823-506-2	Sequence 2, Appli
25	940	31.6	536	9	US-09-776-865-2	Sequence 2, Appli
26	940	31.6	536	16	US-10-823-506-8	Sequence 8, Appli
27	931	31.3	495	9	US-09-776-865-4	Sequence 4, Appli
28	931	31.3	495	16	US-10-823-506-4	Sequence 4, Appli
29	775.5	26.1	493	15	US-10-369-493-5834	Sequence 5834, Ap
30	765.5	25.8	662	15	US-10-425-114-67137	Sequence 67137, A
31	734.5	24.7	591	16	US-10-437-963-160214	Sequence 160214,
32	715.5	24.1	470	16	US-10-767-701-44234	Sequence 44234, A
33	709	23.9	513	15	US-10-424-599-149883	Sequence 149883,
34	636.5	21.4	495	16	US-10-83-506-10	Sequence 10, Appl
35	636.5	21.4	495	16	US-10-823-506-12	Sequence 12, Appl
36	626.5	21.1	467	9	US-09-991-212A-3	Sequence 3, Appli
37	626.5	21.1	467	10	US-09-965-522-3	Sequence 3, Appli
38	626.5	21.1	467	17	US-10-877-818-3	Sequence 3, Appli
39	615	20.7	465	9	US-09-915-181A-8	Sequence 8, Appli
40	576	19.4	445	15	US-10-425-114-64466	Sequence 64466, A
41	561	18.9	284	15	US-10-264-049-2477	Sequence 2477, Ap
42	555.5	18.7	428	16	US-10-437-963-180313	Sequence 180313,
43	530	17.8	272	15	US-10-264-237-2351	Sequence 2351, A
44	489	16.5	283	15	US-10-425-114-47324	Sequence 47324, A
45	488.5	16.4	449	15	US-10-424-599-279212	Sequence 279212,

ALIGNMENTS

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RESULT 1
US-10-314-790-5
; GENERAL INFORMATION:
;  APPLICANT: EMORY UNIVERSITY
;             Gunn, Robert B.
;             Timmer, Richard T.
;  TITLE OF INVENTION: SODIUM-PHOSPHATE COTRANSPORTER IN
;                      LITHIUM THERAPY FOR THE TREATMENT OF MENTAL ILLNESS
;  NUMBER OF SEQUENCES: 12
;  CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Kilpatrick Stockton LLP
;     STREET: Suite 2800, 1100 Peachtree Street NE
;     CITY: Atlanta
;     STATE: GA
;     COUNTRY: USA
;     ZIP: 30309-4530
;  COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;  CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/314,790
;     FILING DATE: 09-Dec-2002
;     CLASSIFICATION: <Unknown>
;  PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/09/380,164
;     FILING DATE: <Unknown>
;     APPLICATION NUMBER: PCT/US98/02875
;     FILING DATE: <Unknown>
;  ATTORNEY/AGENT INFORMATION:
;     NAME: Meredith, Roy D.
;     REGISTRATION NUMBER: 30,777
;     REFERENCE/DOCKET NUMBER: EMU153PCT
;  TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (404) 815-6500
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;   TELEFAX: (404) 815-6555
;   SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-314-790-5

Query Match   99.9%; Score 2967; DB 15; Length 560;
Best Local Similarity 99.8%; Pred. No. 2.7e-258;
Matches 559; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy   1  MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
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Db   1  MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETVELSADGRPVTTQTRDPPVVDCTCFGLP 60

Qy  61  RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
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Qy 121  GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
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Qy 181  LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
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Qy 241  YGSFGIFWYLFWLLVSYESPALHPSISEBERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
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Db 241  YGSFGIFWYLFWLLVSYESPALHPSISEBERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300

Qy 301  SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
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Qy 541  YGATHSTFQPPRPPPVRDY 560
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Db 541  YGATHSTFQPPRPPPVRDY 560
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RESULT 2
US-09-991-212A-4
; Sequence 4, Application US/09991212A
; Patent No. US2002009693A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
            Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
            PHOSPHATE CO-TRANSPORTER
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/991,212A

;   FILING DATE: 16-No.-US2002009693A1-2001
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 09/391,958
;   FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Billings, Lucy J.
;   REGISTRATION NUMBER: 36,749
;   REFERENCE/DOCKET NUMBER: PF-0221 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-855-0555
;   TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 560 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;   LIBRARY: GenBank
;   CLONE: 507415
;   SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-991-212A-4

Query Match   98.5%; Score 2925; DB 9; Length 560;
Best Local Similarity 98.2%; Pred. No. 1.7e-254;
Matches 550; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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Qy   1  MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
           ||||||||||||||||:||||||||||||||||||||||||||:|||||||||||||||
Db   1  MEFRQEEFRKLAGRALGRLHRLLEKRQEGAETLELSADGRPVTTHTRDPPVVDCTCFGLP 60

Qy  61  RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
           |||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db  61  RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFNWDPETVGLIH 120

Qy 121  GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121  GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy 181  LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181  LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy 241  YGSFGIFWYLFWLLVSYESPALHPSISEBERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
           ||||||||||||||||||||||||||||||||||||||||||||:|||:||||||||||
Db 241  YGSFGIFWYLFWLLVSYESPALHPSISEBERKYIEDAIGESAKLMNPVTKFNTPWRRFFT 300

Qy 301  SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
           |||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||
Db 301  SMPVYAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy 361  IADFLRSRRIMSTTNVRKLMNCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
           ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361  IADFLRSRHIMSTTNVRKLMNCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy 421  GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421  GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy 481  GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEABPPGAPPAPPPS 540
           |||||||||||||||||||||||||||:||||||||||:||||:|:|:|||||||||||
Db 481  GGVIFYGVFASGEKQPWAEPEEMSEEKCCGFVGHDQLAGSDESEMBDEVEPPGAPPAPPPS 540

Qy 541  YGATHSTFQPPRPPPVRDY 560
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Db 541  YGATHSTVQPPRPPPVRDY 560
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RESULT 3
US-09-915-181A-5
; Sequence 5, Application US/09915181A
; Patent No. US2002009873A1

GENERAL INFORMATION:
; APPLICANT: EDWARDS, ROBERT
; APPLICANT: BELLOCCHIO, ELIZABETH
; APPLICANT: FREMEAU, ROBERT
; APPLICANT: REIMER, RICHARD
; TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS
; FILE REFERENCE: 305T-93261US
; CURRENT APPLICATION NUMBER: US/09/915,181A
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/220,556
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 560
;   TYPE: PRT
;   ORGANISM: Rattus rattus
US-09-915-181A-5

Query Match   98.5%;   Score 2925; DB 9; Length 560;
Best Local Similarity   98.2%;   Pred. No. 1.7e-254;
Matches 550; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy   1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
Db   1 MEFRQEEFRKLAGRALGRLHRLLEKRQEGAETLELSADGRPVTTHTRDPPVVDCTCFGLP 60

Qy   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
Db   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFNWDPETVGLIH 120

Qy 121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
Db 121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy 181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
Db 181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy 241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
Db 241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPVTKFNTPWRRFFT 300

Qy 301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
Db 301 SMPVYAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy 361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
Db 361 IADFLRSRHIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy 421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
Db 421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Qy 481 GGVIFYGVFASGEKQPWAEPEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPS 540
Db 481 GGVIFYGVFASGEKQPWAEPEMSEEKCGFVGHDQLAGSDESEMEDEVEPPGAPPAPPPS 540

Qy 541 YGATHSTFQPPRPPPPVRDY 560
Db 541 YGATHSTVQPPRPPPVRDY 560

RESULT 4
US-09-965-522-4
; Sequence 4, Application US/09965522
Publication No. US2003022325A1
; GENERAL INFORMATION:
;   APPLICANT: Lal, Preeti
;   Bandman, Olga
;   TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
;   PHOSPHATE CO-TRANSPORTER

INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 560 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: GenBank
;   CLONE: 507415
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-965-522-4

Query Match   98.5%;   Score 2925; DB 10; Length 560;
Best Local Similarity   98.2%;   Pred. No. 1.7e-254;
Matches 550; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy   1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
Db   1 MEFRQEEFRKLAGRALGRLHRLLEKRQEGAETLELSADGRPVTTHTRDPPVVDCTCFGLP 60

Qy   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
Db   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFNWDPETVGLIH 120

Qy 121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
Db 121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

Qy 181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
Db 181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

Qy 241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
Db 241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPVTKFNTPWRRFFT 300

Qy 301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
Db 301 SMPVYAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360

Qy 361 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 420
Db 361 IADFLRSRHIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420

Qy 421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480

Db   421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
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Qy   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDSEMEDEAEPPGAPPAPPPS 540
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Db   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDSESEMEDEVEPPGAPPAPPPS 540
Qy   541 YGATHSTFQPPRPPPVRDY 560
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Db   541 YGATHSTVQPPRPPPVRDY 560

RESULT 5
US-10-877-818-4
; Sequence 4, Application US/10877818
; Publication No. US2005004724A1
; GENERAL INFORMATION:
;   APPLICANT: Lal, Preeti
;   APPLICANT: Bandman, Olga
;   TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT PHOSPHATE COTRANSPORTER
;   FILE REFERENCE: 11669.126USC1
;   CURRENT APPLICATION NUMBER: US/10/877,818
;   CURRENT FILING DATE: 2004-06-25
;   PRIOR APPLICATION NUMBER: US 09/965,522
;   PRIOR FILING DATE: 2001-09-26
;   PRIOR APPLICATION NUMBER: US 09/391,958
;   PRIOR FILING DATE: 1999-09-08
;   PRIOR APPLICATION NUMBER: US 08/805,118
;   PRIOR FILING DATE: 1997-02-24
;   NUMBER OF SEQ ID NOS: 7
;   SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
;   LENGTH: 560
;   TYPE: PRT
;   ORGANISM: Rat
US-10-877-818-4

  Query Match   98.5%; Score 2925; DB 17; Length 560;
  Best Local Similarity   98.2%; Pred. No. 1.7e-254;
  Matches 550; Conservative   5; Mismatches   5; Indels   0; Gaps   0;

Qy   1 MEFRQEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLP 60
         |||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db   1 MEFRQEEFRKLAGRALGRLHRLLEKRQEGAETLELSADGRPVTTHTRDPPVVDCTCFGLP 60
Qy   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIH 120
         ||||||||||||||||||||||||||||||||||||||:||||||||||:||||||||||
Db   61 RRYIIAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFNWDPETVGLIH 120
Qy   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRIIQG 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRIIQG 180
Qy   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
Qy   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFT 300
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Db   241 YGSFGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPVTKFNTPWRRFFT 300
Qy   301 SMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 SMPVYAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQ 360
Qy   361 IADFLRSRRIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 IADFLRSRHIMSTTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAIS 420
Qy   421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
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Db   421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHY 480
Qy   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDSEMEDEAEPPGAPPAPPPS 540

Db   481 GGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDSESEMEDEVEPPGAPPAPPPS 540
Qy   541 YGATHSTFQPPRPPPVRDY 560
         |||||| |||||||||||||
Db   541 YGATHSTVQPPRPPPVRDY 560

RESULT 6
US-09-740-041-4
; Sequence 4, Application US/09740041
; Patent No. US2002082190A1
; GENERAL INFORMATION:
;   APPLICANT: MERKULOV, Karl et al
;   TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
;   TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: CL001001
;   CURRENT APPLICATION NUMBER: US/09/740,041
;   CURRENT FILING DATE: 2000-12-20
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 578
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-09-740-041-4

  Query Match   77.9%; Score 2313.5; DB 9; Length 578;
  Best Local Similarity   79.3%; Pred. No. 2.3e-199;
  Matches 428; Conservative   57; Mismatches 50; Indels   5; Gaps   2;

Qy   5 QEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLPRRYI 64
         :||:|| ||:::|:|:||: : |||:| |::|:   :::|:: : ::|||:||||||
Db   12 KEGIKNFAGKSLGQIYRVLEKKQDNRETELTEDGKPLEVPEKKAPLCDCTCFGLPRRYI 71
Qy   65 IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFF 124
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Db   72 IAIMSGLGFCISFGIRCNLGVAIVDMVNNSTIHRGGKVIKEKAKFNWDPETVGMIHGSFF 131
Qy   125 WGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRIIQGLVEG 184
         |||||||||||||: |:|:|||||:||||||||||||||||||||||:|||||||||||
Db   132 WGYIITQIPGGYIASRLAANRVFGAAILJTSTLNMLIPSAARVHYGCVIFVRILQGLVEG 191
Qy   185 VTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYVYGSF 244
         ||||||||||||||||||||||||:|||||||||:||||||:|||||:||:|||:||||
Db   192 VTYPACHGIWSKWAPPLERSRLATTSFCGSYAGAVIAMPLAGIVQYTGWSSVFVVYGSF 251
Qy   245 GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPV 304
         |: | ||:|||||||| |||:: : :|||:||:: |:|||:| :|| ||:||||||
Db   252 GMWVWMFWLLVSYESPAKHPTITDERRYIEESIGESANLLGAMEKFKIPWRKFFTSMPV 311
Qy   305 YAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADF 364
         ||||||||||||||||||||||| |||||||||||||||:||:|||||||||||||||||
Db   312 YAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGMLSAVPHLVMTIIVPIGGQIADF 371
Qy   365 LRSRRIMSTNVRKLMNCCGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGFNV 424
         |||: ::::|||||||:||||||||||||||||||||||||||||||||||:||||||||
Db   372 LRSKQILSTTTVRKIMNCCGFGMEATLLLVVGYSHTRGVAISFLVLAVGFSGFAISGFNV 431
Qy   425 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVI 484
         ||||||||||||||||||||||||||||||||:||||||||||||||||||:||||||||
Db   432 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKNKSREEWQYVFLIAALVHYGGVI 491
Qy   485 FYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDSEMEDEAEPPGAPPAPPPSYGAT 544
         |:|||||||||||| |: :||||||||||||||||||: : | :||||
Db   492 FYALFASGEKQPWADPEETSEEKCGFIHEDEL----DEETGDITQ-NYINVGTTKSYGAT 546

RESULT 7
US-10-389-967-4
; Sequence 4, Application US/10389967
; Publication No. US20030166153A1

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; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001001-DIV
; CURRENT APPLICATION NUMBER: US/10/389,967
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
US-10-389-967-4
; SEQ ID NO 4
; LENGTH: 578
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-389-967-4

Query Match            77.9%;  Score 2313.5;  DB 14;  Length 578;
Best Local Similarity  79.3%;  Pred. No. 2.3e-199;
Matches  428;  Conservative  57;  Mismatches  50;  Indels  5;  Gaps  2;

Qy     5 QEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLPRRYI 64
           :|: |||:|::|||::||||  ||:|: ||:|:  :|||||||||||
Db    12 KEGIKNFAGKSLGQIYRVLEKKQDNRETIELTEDGKPLEVPEKKAPLCDCTCFGLPRRYI 71

Qy    65 IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFF 124
           |||||||||||||||||||||||||||||||  ||| ::  : |||||||||||||||
Db    72 IAIMSGLGFCISFGIRCNLGVAIVDMVNNSTIHRGGKVIKEKAKFNWDPETVGMIHGSFF 131

Qy   125 WGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEG 184
           ||||||||||||| ||:|||||:|||:|||||||||||||||||||||||||||||||
Db   132 WGYIITQIPGGYIASRLAANRVFGAAILLTSTLNMLIPSAARVHYGCVIFVRILQGLVEG 191

Qy   185 VTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVAMPLAGVLVQYSGWSSVFYVYGSF 244
           ||||||||||||||||||||||:|::|||||||||||:|||||:|:|||:|||||||
Db   192 VTYPACHGIWSKWAPPLERSRLATTSFCGSYAGAVIAMPLAGIIVQYTGWSSVFYVYGSF 251

Qy   245 GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPV 304
           |:|:|||||||||:||:||||::  ::||||:||||||::|||| |||||::||||||
Db   252 GMVWYMFWLLVSYESPAKHPTITDEERRYIEESIGESANLLGAMEKFKTPWRKFFTSMPV 311

Qy   305 YAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADF 364
           |||||||||||||||||||||||  |||||||||||||:|:|||||||||||||||||||
Db   312 YAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGMLSAVPHLVMTIIVPIGGQIADF 371

Qy   365 LRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGFNV 424
           |||::| |::|||||||||||||||||||||||:||  ||||||||||||||||||||||
Db   372 LRSKQILSTTTVRKIMNCGGFGMEATLLLVVGYSHTRGVAISFLVLAVGFSGFAISGFNV 431

Qy   425 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVI 484
           ||||||||||||||||||||||||||||||||||:|:: ||||||||||:||| |||||||
Db   432 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKNKSREEWQYVFLIAALVHYGGVI 491

Qy   485 FYGVFASGEKQPWAEPEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPSYGAT 544
           |||:|||||||||| ||::||||||  ||||||||:||||||||:|| |||| ||||||
Db   492 FYALFASGEKQPWADPEETSEEKCGFIHEDEL----DEETGDITQ-NYINYGTTKSYGAT 546


RESULT 8
US-09-915-181A-4
; Sequence 4, Application US/09915181A
; Patent No. US2002009847341
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ROBERT
; APPLICANT: BELLOCCHIO, ELIZABETH
; APPLICANT: FREMEAU, ROBERT
; APPLICANT: REIMER, RICHARD
; TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS
; FILE REFERENCE: 305T-93261OUS
; CURRENT APPLICATION NUMBER: US/09/915,181A
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/220,556
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 11
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-915-181A-4

Query Match            77.9%;  Score 2313.5;  DB 9;  Length 582;
Best Local Similarity  79.3%;  Pred. No. 2.3e-199;
Matches  428;  Conservative  57;  Mismatches  50;  Indels  5;  Gaps  2;

Qy     5 QEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLPRRYI 64
Db    13 KEGIKNFAGKSLGQIYRVLEKKQDNRETIELTEDGKPLEVPEKKAPLCDCTCFGLPRRYI 72

Qy    65 IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFF 124
Db    73 IAIMSGLGFCISFGIRCNLGVAIVDMVNNSTIHRGGKVIKEKAKFNWDPETVGMIHGSFF 132

Qy   125 WGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEG 184
Db   133 WGYIITQIPGGYIASRLAANRVFGAAILLTSTLNMLIPSAARVHYGCVIFVRILQGLVEG 192

Qy   185 VTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVAMPLAGVLVQYSGWSSVFYVYGSF 244
Db   193 VTYPACHGIWSKWAPPLERSRLATTSFCGSYAGAVIAMPLAGIIVQYTGWSSVFYVYGSF 252

Qy   245 GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPV 304
Db   253 GMWYMFWLLVSYESPAKHPTITDEERRYIEESIGESANLLGAMEKFKTPWRKFFTSMPV 312

Qy   305 YAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADF 364
Db   313 YAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGMLSAVPHLVMTIIVPIGGQIADF 372

Qy   365 LRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGFNV 424
Db   373 LRSKQILSTTTVRKIMNCGGFGMEATLLLVVGYSHTRGVAISFLVLAVGFSGFAISGFNV 432

Qy   425 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVI 484
Db   433 NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKNKSREEWQYVFLIAALVHYGGVI 492

Qy   485 FYGVFASGEKQPWAEPEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPSYGAT 544
Db   493 FYALFASGEKQPWADPEETSEEKCGFIHEDEL----DEETGDITQ-NYINYGTTKSYGAT 547


RESULT 9
US-10-205-331-7
; Sequence 7, Application US/10205331
; Publication No. US20040058326A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brookabank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018199
; CURRENT APPLICATION NUMBER: US/10/205,331
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Differentiation-associated Na-dependent inorganic phosphate cotra
US-10-205-331-7
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Query Match      77.9%;  Score 2313.5;  DB 15;  Length 582;
Best Local Similarity   79.3%;  Pred. No. 2.3e-199;
Matches  428;  Conservative  57;  Mismatches  50;  Indels   5;  Gaps   2;

Qy      5  QEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLPRRYI   64
           :| ||::||:::| :| :: :| :|: |::: : | ||  ||||||
Db     13  KEGIKNFAGKSLGQYRVLEKKQDNRETIELTEDGKPLEVPEKKAPLCDCTCFGLPRRYI   72

Qy     65  IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFF  124
           ||||||||||||||||||||  |||:|||||||||| || ||||||||||||||||
Db     73  IAIMSGLGFCISFGIRCNLGVAIVDMVNNSTIHRGGKVIKEKAKFNWDPETVGMIHGSFF  132

Qy    125  WGYIVTQIPGGFICQKFAANRVFGAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEG  184
           ||||:||||||| | |:||||||||| ||||::||| ||||||||||||||
Db    133  WGYIITQIPGGYIASRLAANRVFGAAILLTSTLNMLIPSAARVHYGCVIFVRILQGLVEG  192

Qy    185  VTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYVYGSF  244
           ||||| |||||||||||||||||||||:| | |:|| ||||:|:|:||:|||:||
Db    193  VTYPACHGIWSKWAPPLERSRLATTSFCGSYAGAVIAMPLAGILVQYTGWSSVFYVYGSF  252

Qy    245  GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPV  304
           | :||:|:||| |:::| :| :| ::: :|  : ||
Db    253  GMVWYMFWLLVSYESPAKHPTITDEERRYIEESIGESANLLGAMEKFKTPWRKFFTSMPV  312

Qy    305  YAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADF  364
           |||||||||||||||||||||| | ||||||||:|| ||||||||||||||||||||
Db    313  YAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGMLSAVPHLVMTIIVPIGGQIADF  372

Qy    365  LRSRRIMSTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFIVLAVGFSGFAISGFNV  424
           ||:: |||:|||:|||||||||||||||||||:: |||||||:||||:|:||||
Db    373  LRSKQILSTTTVRKIMNCGGFGMEATLLLVVGYSHTRGVAISFIVLAVGFSGFAISGFNV  432

Qy    425  NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVI  484
           |||||||||||||||||||||||||||||||||||::|:||::| |||||:| |||||
Db    433  NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKNKSREEWQYVFLIAALVHYGGVI  492

Qy    485  FYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPSYGAT  544
           |||  ||||||||| :|  |:||||| | ||| :||
Db    493  FYALFASGEKQPWADPEETSEEKCGFIHDEL---DEETGDITQ-NYINYGTTKSYGAT    547
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RESULT 10
US-09-740-041-2
; Sequence 2, Application US/09740041
; Patent No. US2002008190A1
; GENERAL INFORMATION:
;   APPLICANT: MERKULOV, Karl et al
;   TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
;   TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: CL001001
;   CURRENT APPLICATION NUMBER: US/09/740,041
;   CURRENT FILING DATE: 2000-12-20
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 2
;   LENGTH: 589
;   TYPE: PRT
;   ORGANISM: Human
US-09-740-041-2

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Query Match      73.6%;  Score 2185;  DB 9;  Length 589;
Best Local Similarity   76.3%;  Pred. No. 8.8e-188;
Matches  412;  Conservative  53;  Mismatches  69;  Indels   6;  Gaps   3;

Qy      5  QEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLPRRYI   64
           :| |: | ||::||:||||| | :::: ::|:||::||
Db     18  KEGVKNAVGDSLGLIQRKIDGTTEEDNIELNEEGRPVQTSRSPPLCDCHCCGLPKRYI    77

Qy     65  IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFF  124
           |||||||||||||||||||||| ::|:|||||| || |:|| :|| |::||||||||
Db     78  IAIMSGLGFCISFGIRCNLGVAIVEMVNNSTVYDGKPEIQTAQFNWDPETVGLIHGSFF  137
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Qy    125  WGYIVTQIPGGFICQKFAANRVFGAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEG  184
           ||||:||||||| | |:||||||||| ||||::||| |||||||||||||||
Db    138  WGYIMTQIPGGFISNKFAANRVFGAAIFLTSTLNMFIPSAARVHYGCVMCVRILQGLVEG  197

Qy    185  VTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYVYGSF  244
           ||||| |||||||||||||||||||:|| | |:||  ||| |:|:|:|| |||:||
Db    198  VTYPACHGMWSKWAPPLERSRLATTSFCGSYAGAVAMPLAGVLVQYIGWSSVFYIYGMF  257

Qy    245  GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPV  304
           || ||:| || | |:||  :| :| ::: :|:  || |::| |||||
Db    258  GIIWYMFWLLQAYECPAAHPTISNEEKTYIETSIGEGANVVS-LSKFSTPWKRFFTSLPV  316
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RESULT 11
US-10-389-967-2
; Sequence 2, Application US/10389967
; Publication No. US20030166153A1
; GENERAL INFORMATION:
;   APPLICANT: MERKULOV, Karl et al
;   TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
;   TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
;   TITLE OF INVENTION: AND USES THEREOF
;   FILE REFERENCE: CL001001-DIV
;   CURRENT APPLICATION NUMBER: US/10/389,967
;   CURRENT FILING DATE: 2003-03-18
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 2
;   LENGTH: 589
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-389-967-2

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Query Match      73.6%;  Score 2185;  DB 14;  Length 589;
Best Local Similarity   76.3%;  Pred. No. 8.8e-188;
Matches  412;  Conservative  53;  Mismatches  69;  Indels   6;  Gaps   3;

Qy      5  QEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLPRRYI   64
           :| |: | ||::||:||||| | :::: ::|:||::||
Db     18  KEGVKNAVGDSLGLIQRKIDGTTEEDNIELNEEGRPVQTSRSPPLCDCHCCGLPKRYI    77

Qy     65  IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFF  124
           |||||||||||||||||||||| ::|:|||||| || |:|| :|| |::||||||||
Db     78  IAIMSGLGFCISFGIRCNLGVAIVEMVNNSTVYDGKPEIQTAQFNWDPETVGLIHGSFF  137

Qy    125  WGYIVTQIPGGFICQKFAANRVFGAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEG  184
           ||||:||||||| | |:||||||||| ||||::||| |||||||||||||||
Db    138  WGYIMTQIPGGFISNKFAANRVFGAAIFLTSTLNMFIPSAARVHYGCVMCVRILQGLVEG  197

Qy    185  VTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYVYGSF  244
           ||||| |||||||||||||||||||:|| | |:||  ||| |:|:|:|| |||:||
Db    198  VTYPACHGMWSKWAPPLERSRLATTSFCGSYAGAVAMPLAGVLVQYIGWSSVFYIYGMF  257

Qy    245  GIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPV  304
           || ||:| || | |:||  :| :| ::: :|:  || |::| |||||
Db    258  GIIWYMFWLLQAYECPAAHPTISNEEKTYIETSIGEGANVVS-LSKFSTPWKRFFTSLPV  316
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Qy  420  SGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVH  479
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Db  445  SGFNVNHDIAPRYASILMGISNGVGTLSGMVCPLIVGAMTKHKTREEWQNVFLIAALVH  504

Qy  480  YGGVIFYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPP  539
              |.||||||||||||| |*.|:||:||||||..|||:|    ::   |*       |::
Db  505  YSGVIFYGVFASGEKQDWADPENLSEEKCGIIDQDELA---EETELNHEA---FVSPRKM  559

Qy  540  SYGAT  544
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Db  560  SYGAT  564
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RESULT 13
US-10-287-226-300
; Sequence 300, Application US/10287226
; Publication No. US2004008675A1
; GENERAL INFORMATION:
;   APPLICANT: Agee, Michele L.,
;   APPLICANT: Alsobrook, John P.,
;   APPLICANT: Berghs, Constance,
;   APPLICANT: Boldog, Ference,
;   APPLICANT: Burgess, Catherine E.,
;   APPLICANT: Chant, John S.,
;   APPLICANT: Chaudhuri, Amitabha,
;   APPLICANT: DiPippo, Vincent A.,
;   APPLICANT: Edinger, Shlomit R.,
;   APPLICANT: Eisen, Andrew,
;   APPLICANT: Ellerman, Karen,
;   APPLICANT: Gangolli, Esha A.,
;   APPLICANT: Gorman, Linda,
;   APPLICANT: Gerlach, Valerie,
;   APPLICANT: Ji, Weizhen,
;   APPLICANT: Kekuda, Ramesh,
;   APPLICANT: Khramtsov, Nikolai,
;   APPLICANT: Li, Li,
;   APPLICANT: Malyankar, Uriel M.,
;   APPLICANT: MacDougall, John R.,
;   APPLICANT: Mezes, Peter S.,
;   APPLICANT: Miller, Charles E.,
;   APPLICANT: Millet, Isabelle,
;   APPLICANT: Ooi, Chean Eng,
;   APPLICANT: Ort, Tatiana,
;   APPLICANT: Padigaru, Muralidhara,
;   APPLICANT: Patturajan, Meera,
;   APPLICANT: Rastelli, Luca,
;   APPLICANT: Rieger, Daniel K.,
;   APPLICANT: Rothenberg, Mark E.,
;   APPLICANT: Shenoy, Suresh G.,
;   APPLICANT: Spaderna, Steven K.,
;   APPLICANT: Spytek, Kimberley A.,
;   APPLICANT: Taupier, Jr., Raymond J.,
;   APPLICANT: Vernet, Corine A.M.,
;   APPLICANT: Zerhusen, Bryan D.,
;   APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-480C
; CURRENT APPLICATION NUMBER: US/10/287,226
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: 60/334,421
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,392
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/360,148
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/364,000
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/404,821
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/334,526
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,409
; PRIOR FILING DATE: 2002-02-04

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Qy  305  YAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADF  364
              ||||||||||||||||||||||||:||||||||:||||||||||||||||||||||
Db  317  YAIIVANFCRSWTFYLLLISQPAYFEEVFGFAISGFNV                        376

Qy  365  LRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGFNV  424
              ||||:|:.||.||||||||||||||||||||.||:|||||||||||||||||||||||
Db  377  LRSRQILTTTAVRKIMNCGGFGMEATLLLVVGFSHTKGVAISFLVLAVGFSGFAISGFNV  436

Qy  425  NHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVI  484
              ||||||||||||||||||||||||||||||:||||||:||||||||:||||| ||||.||
Db  437  NHLDIAPRYASILMGISNGVGTLSGMVCPLIVGAMTRHKTREEWQNVFLIAALVHYSGVI  496

Qy  485  FYGVFASGEKQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPPAPPPSYGAT  544
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Db  497  FYGVFASGEKQEWADPENLSEEKCGIIDQDELA--EEIELNHES---FASPKKKMSYGAT  551
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RESULT 12
US-09-915-181A-3
; Sequence 3, Application US/09915181A
; Patent No. US20020098473A1
; GENERAL INFORMATION:
;   APPLICANT: EDWARDS, ROBERT
;   APPLICANT: BELLOCCHIO, ELIZABETH
;   APPLICANT: FREMEAU, ROBERT
;   APPLICANT: REIMER, RICHARD
; TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS
; FILE REFERENCE: 305T-93261US
; CURRENT APPLICATION NUMBER: US/09/915,181A
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/220,556
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
;   LENGTH: 850
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-915-181A-3

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Query Match              73.2%;  Score 2174.5;  DB 9;  Length 850;
Best Local Similarity    76.0%;  Pred. No. 1.3e-186;
Matches   414;  Conservative  51;  Mismatches  69;  Indels  11;  Gaps   5;

Qy    5  QEEFRKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLPRRYI   64
              ::| :|::|  ||:| ||:::::..|| :|||::.||||:|.|   || ||:| |:|||
Db   26  KEGVKNAVGDSLGILQRKLDGTNEEGDAIELSEEGRPVQTSRARAPVCDCSCCGIPKRYI   85

Qy   65  IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTHRGGHVVVVQKAQFSWDPETVG----LIH  120
              ||:|||||||||||||||||||||.|||||||.  |:.|.:.||:.||||||    |||
Db   86  IAVMSGLGFCISFGIRCNLGVAIVEMVNNSTVYVDGKPEIQTAQFNWDPETVGRANSLIH  145

Qy  121  GSFFWGYIVTQIPGGFICQKFAANRVFGAAIVATSTINMLIPSAARVHYGCVIFVRILQG  180
              ||||||||||||||||| .||||||||||||| :||:||:|||||||||||:.||||||
Db  146  GSFFWGYIVTQIPGGFISNKFAANRVFGAAIFLTSTLNMFIPSAARVHYGCVMCVRILQG  205

Qy  181  LVEGVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV  240
              |||||||||||.:||||||||||||||||:||||||||||||||||||||:||.|:|:|:
Db  206  LVEGVTYPACHGMWSKWAPPLERSRLATTSFCGSYAGAVVAMPLAGVLVQYIGWASAFYI  265

Qy  241  YGSFGIFWYLFWLLV-SYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFF  299
              ||.||:.||:||||| ::|..|.|| ||.||:.||| :||| | :|: *:|::.||||||
Db  266  YGMFGIIWYMFWLLLQAYECPAVHPTISNEERTYIETSIGEGANLAS-LSKFNTPWRRFF  324

Qy  300  TSMPVYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGG  359
              ||:||||||||||||||||||||||||:||||||||:||||||:||:||:||||||||||
Db  325  TSLPVYAIIVANFCRSWTFYLLLISQPAYFEEVFGFAISKVGLLSAVPHMVMTIIVPIGG  384

Qy  360  QIADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAI  419
              |:||:||||:|:.||.||||||||||||||||||||.||:|||||||||||||||||||
Db  385  QLADYLRSRKILTTTAVRKIMNCGGFGMEATLLLVVGFSHTKGVAISFLVLAVGFSGFAI  444
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us-10-734-731-4.rapb

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; PRIOR APPLICATION NUMBER: 60/364,227
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/334,027
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/331,641
; PRIOR FILING DATE: 2001-11-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 673
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 300
;   LENGTH: 566
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-287-226-300

Query Match          72.0%;   Score 2138.5;  DB 15;  Length 566;
Best Local Similarity  76.6%;  Pred. No. 1.3e-183;
Matches   407;  Conservative   51;  Mismatches   56;  Indels   17;  Gaps    6;

Qy    14  RALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDPPVVDCTCFGLPRRYIIAIMSGLGF   73
          :||:: ||||||||||||||||         || :||:| ||:||||||||||||||
Db    15  KSMGQL------REE--DNIELNEEGRPVQTSRPSPPLCDCHCCGLPKRYIIAIMSGLGF   66

Qy    74  CISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFFWGYIVTQIP  133
          ||||||||||||||||||||||||||||         | |||||||||||||||||||||
Db    67  CISFGIRCNLGVAIVEMVNNSTVYVDGK---QTAQFNWDPETVGLIHGSFFWGYIMTQIP  123

Qy   134  GGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEGVTYPACHGI  193
          |||| ||| |||||||||||| ||||||||||||||||:  |||||||||||||||||
Db   124  GGFISNKFAANRVFGAAIFLTSTLNMFIPSAARVHYGCVMCVRILQGLV-GVTYPACHGM  182

Qy   194  WSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYVVYGSFGIFWYLFWL  253
          ||||||||||||||||||||||||||||||||||||||||||||:  |||||:
Db   183  WSKWAPPLERSRLATTSFCGSYAGAVVAMPLAGVLVQYIGWSSVFYIYGMFGIIWYMFWL  242

Qy   254  LVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMPVYAIIVANFC  313
          |||:||||||||||||||||||||||||        | ::| ||||||||:| |||||||
Db   243  LQAYECPAAHPTISNEEKTYIETSIGEGANVVSLSVKFSTPWKRFFTSLPVYAIIVANFC  302

Qy   314  RSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIADFLRSRRIMST  373
          ||||||||||||||||||||||||:||::||||||||||:|||||||||||:|:|:|:|
Db   303  RSWTFYLLLISQPAYFEEVFGFAISKVGLLSAVPHMVMVIVVPIGGQLADYLRSRQILTT  362

Qy   374  TNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGFNVNHLDIAPRY  433
          | |||:||:|||||||||||||||||||||||||||||||||||||||||||:|||||||
Db   363  TAVRKIMNCGGFGMEATLLLVVGFSHTKGVAISFLVLAVGFSGFAISGFNVNHIDIAPRY  422

Qy   434  ASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGVIFYGVFASGE  493
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   423  ASILMGISNGVGTLSGMVCPLIVGAMTRHKTREEWQNVFLIAALVHYSGVIFYGVFASGE  482

Qy   494  KQPWAEPEEMSEEKCGFVGHDQLAGSDDSEMEDEAEPPGAPAPPPSYGAT  544
          || |  ||| ||||||||||        :: |:   |||
Db   483  KQEWADPENLSEBKCGIIDQDELA--EBIELNHES---FASPKKKMSYGAT  528
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RESULT 14
US-10-014-079A-1
; Sequence 1, Application US/10014079A
; Publication No. US20030017479A1
; GENERAL INFORMATION:
;   APPLICANT: Kaplan, Joshua M.
;   APPLICANT: Oppenheimer, Allison J.
;   APPLICANT: Hart, Anne C.
;   TITLE OF INVENTION: METHODS FOR THE DETECTION, TREATMENT,
;   TITLE OF INVENTION: AND PREVENTION OF NEURODEGENERATION
;   FILE REFERENCE: 00786/353002
;   CURRENT APPLICATION NUMBER: US/10/014,079A
;   CURRENT FILING DATE: 2002-09-10
;   PRIOR APPLICATION NUMBER: US 08/864,785
;   PRIOR FILING DATE: 1997-05-29
;   NUMBER OF SEQ ID NOS: 3
;   SOFTWARE: FastcSEQ for Windows Version 4.0
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; SEQ ID NO 1
;   LENGTH: 576
;   TYPE: PRT
;   ORGANISM: Caenorhabditis elegans
US-10-014-079A-1

Query Match          43.7%;   Score 1297;  DB 14;  Length 576;
Best Local Similarity  47.7%;  Pred. No. 9.2e-108;
Matches   262;  Conservative   88;  Mismatches   171;  Indels   28;  Gaps   10;

Qy     9  RKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDP---PVVDCTCFGLPR-RYI   64
          :||:: ||||||||||||||||||||||       ||| :||:            | ::|
Db    12  KQMVGEPLAKMTAAAASATGAAPPQOMQEBGNENPMQMHSNKVLQVMEQTWIGKCRKRWL   71

Qy    65  IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTTHRGGHVVVQKAQFSWDPETVGLIHGSFF  124
          |||||||:|:||||||||||||||||||||||||||         ::|||:| :|||||:
Db    72  LAILANMGFMISFGIRCNFGAAKTHMYKNYTDPYG---KVHMHEFNWTIDELSVMESSYF  128

Qy   125  WGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYG-CVIFVRILQGLVE  183
          :||:|||||||||         ||||||||||||||||||||||||  :|||:||||||
Db   129  YGYLVTQIPAGFLAAKFPPNKLPGFGIGVGAFLNILLPYGFKVKSDYLVAFIQITQGLVQ  188

Qy   184  GVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYVVYGS  243
          ||||| |  |||||||||||||||||| ||||||||||:||||||||||||||||| ||
Db   189  GVCYPAMHGVGWRYWAPPMERSKLATTAFTGSYAGAVLGLPLSAFLVSYVSWAAPFLYGV  248

Qy   244  FGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFFTSMP  303
          |||| ||||||||: :|| |||||||:|||||||||| :|||| :||:|:|        |
Db   249  CGVIWAILWFCVTFEKPAFHPTISQEEKIFIEDAIGHVSN-THPTIR-SIPWKAIVTSKP  306

Qy   304  VYAIIVANFCRSWTFYLLLISQPDYFEEVFGFEISKVGLVSALPHLVMTIIVPIGGQIAD  363
          |:||||||||||||||||||||||||||||||||:||:||||::||:||||||||||||:
Db   307  VWAIIVANFARSWTFYLLLQNQLYMKEALGMKIADSGLLAAIPHLVMGCVLMGGQLAD  366

Qy   364  FLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGFSGFAISGFN  423
          :|||::|||:|||||||||||||||||||||:|||||||||::|| || ||:|||||||||
Db   367  YLRSNKILSTTAVRKIFNCCGFGGEAAFMLIVAYTTSDTTAIMALIAAVGMSGFAISGFN  426

Qy   424  VNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGV  483
          |||||||||||:||||||| :|||||||||||||||:|:||:|||||:||||||||||
Db   427  VNHLDIAPRYAAILMGFSNGIGTLAGLTCPFVTEAFTAH-SKHGWTSVFLLASLIHFTGV  485

Qy   484  IFYGVFASGEKQPWAEPEEMSE--------EKCGFVG----------HDQLAGSDDSEMEDE  527
          |||||||||  |: |                ||||:
Db   486  TFYAVYASGELQEWAEPKEEEWSNKELVNKTGTNGTGYGAAETTFTQLPAGVDSSYQAQ  545

Qy   528  AEP-PGAPP  535
          | : ||
Db   546  AAPAPGTNP  554
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```
RESULT 15
US-10-369-493-5823
; Sequence 5823, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
;   APPLICANT: Cao, Yongwei
;   APPLICANT: Hinkle, Gregory J.
;   APPLICANT: Slater, Steven C.
;   APPLICANT: Goldman, Barry S.
;   APPLICANT: Chen, Xianfeng
;   TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
;   TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
;   FILE REFERENCE: 38-10(52052)B
;   CURRENT APPLICATION NUMBER: US/10/369,493
;   CURRENT FILING DATE: 2003-02-28
;   PRIOR APPLICATION NUMBER: US 60/360,039
;   PRIOR FILING DATE: 2002-02-21
;   NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5823
;   LENGTH: 576
;   TYPE: PRT
;   ORGANISM: Caenorhabditis elegans
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Thu Jun 2 13:29:03 2005

us-10-734-731-4.rapb

US-10-369-493-5823

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Query Match            43.7%;  Score 1297;  DB 15;  Length 576;
Best Local Similarity  47.7%;  Pred. No. 9.2e-108;
Matches  262;  Conservative  88;  Mismatches 171;  Indels  28;  Gaps  10;

Qy      9 RKLAGRALGKLHRLLEKRQEGAETLELSADGRPVTTQTRDP---PVVDCTCFGLPR-RYI  64
            ::||::    |||||||||||||:|:|: |||           |::|| |||::  :|:
Db     12 KQMVGEPLAKMTAAAASATGAAPPQQMQEEGNENPMQMHSNKVLQVMEQTWIGKCRKRWL  71

Qy     65 IAIMSGLGFCISFGIRCNLGVAIVSMVNNSTHRGGHVVVQKAQFSWDPETVGLIHGSFF 124
          :|||:|||:.:|||||||||||||||    |   |        | ::|    ||: :|:|
Db     72 LAILANMGFMISFGIRCNFGAAKTHMYKNYTDPYG---KVHMHEFNWTIDELSVMESSYF 128

Qy    125 WGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYG-CVIFVRILQGLVE 183
          :||::||||||| |  ||  |: ||| |  |::|::|||  :| || :|:|||: ||||:
Db    129 YGYLVTQIPAGFLAAKPPPNKLFGFGIGVGAFLNILLPYGFKVKSDYILVAFIQITQGLVQ 188

Qy    184 GVTYPACHGIWSKWAPPLERSRLATTAFCGSYAGAVAMPLAGVLVQYSGWSSVFVVYGS 243
          || |||  ||| ||  || ::|||||| ||||||||||||||| : |||:||:|| :|:
Db    189 GVCYPAMHGVWRYWAPPMERSKLATTAFTGSYAGAVLGLPLSAFLVSYVSWAAPFYLYGV 248

Qy    244 FGIFWYLFWLLVSYESPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPWRRFPTSMP 303
          | |:||| | |||| |||||  |:|:|::|||||:|:::|||| |||: :|| : ||: |
Db    249 CGVIWAILWFCVTFEKPAFHPTISQEEKIFIEDAIGHVSN-THPTIR-SIPWKAIVTSKP 306

Qy    304 VYAIIVANFCRSWTFYLLISQPDYFPEVFGFEISKVGLVSALPHLVMTIIVPIGGQIAD 363
          ::||||||| |:||||||||:|| ||  | |||: || ||| :|:|||:|||||:|||||
Db    307 VWAIIVANFARSWTFYLLLQNLTYMKEALGMKIADSGLLAAIPHLVMGCVVLMGGQLAD 366

Qy    364 FLRSRRIMSTTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAVGPSGFAISGFN 423
          ::||| :|::|||: |||||||||: ||:::|||:|:|||:: |:| ||| ||||||||||
Db    367 YLRSNKILSTTAVRKIFNCGGFGGEAAFMLIVAYTTSDTTAIMALIAAVGMSGFAISGFN 426

Qy    424 VNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREEWQYVFLIASLVHYGGV 483
          |||||||||||::|||:|||||||:||| :||:| |:||| :   |||:||:|||||| |
Db    427 VNHLDIAPRYAAILMGFSNGIGTLAGLTCPFVTEAFTAH-SKHGWTSVFLLASLIHFTGV 485

Qy    484 IFYGVFASGEKQPWAEPEEMSE-------EKCGFVG--------HDQLAGSDDSEMEDE 527
          ||:|:||||:| |  |  |||:         |||:|        :
Db    486 TFYAVYASGELQEWAEPKEEEEWSNKELVNKTGINGTGYGAAETTFQLPAGVDSSYQAQ 545

Qy    528 AEP-PGAPP 535
          |   ||| |
Db    546 AAPAPGTNP 554
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Search completed: June 2, 2005, 11:44:28
Job time : 142 secs